

```

GCCGCCGCCA ACACGCCGAA TGCCGAGCCG GGGGATCCCA ACACGACACC TCCGCCGCCC 300
GACCCGAACG CACCGCCGCC ACCTGTCTTT GCGCCAAACG CACCCCAACC TGTCCGGATC 360
GACACCCCGG TTGGAGGATT CAGCTTCGCG CTGCTCTCTG GCTGGGTGGA GTCTGACGCC 420
GCCCACTTCG ACTACGGTTC AGCACTCTTC AGCAAAACCA CCGGGGACCC GCCATTTCGC 480
GGACAGCCCG CCGCGGTGCG CAATGACACC CGTATCTGTC TCGGCCGGCT AGACCAAAAG 540
CTTTAGCCCA GCGCCGAAGC CACCGACTCC AAGGCCGCGG CCGCGTTGGG CTCGACATG 600
GGTGAAGTTT ATATGCCCTA CCGCGGACCC CGGATCAACC AGGAAACCGT CTCGCTCGAC 660
GCCACCGGGG TGTCTGGAAG CGCTCTGAT TACGAAGTCA AGTTGACGGA TCCGAGTAAG 720
CCGAACGCCC AGATCTGACG GCGCGTAATC GGCTGCGCCG CCGCGAACCC ACCGACGCGC 780
GGGCCCCCTC AGCGCTGGTT TGTGTATGG CTGCGGACCC CCAACAACCC GGTGACACAG 840
GGGCGGCCCA AGCGCTGCGC CGAATCGATC CCGCGTTTGG TCGCCCGGCC CCGCGCGCGG 900
GCACCGGCTC CTGACAGACC CGCTCGCGCG CCGCGCGCGG CCGCGGAAGT CGCTCTTACC 960
CGACAGACAC CGACACCGCA GCGACCTTA CCGCGCTGA 999

```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
 1             5             10             15

Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
 20             25             30

Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
 35             40             45

Gln Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
 50             55             60

Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
 65             70             75             80

Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
 85             90             95

Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro

```

100	105	110
Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser 115	120	125
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp 130	135	140
Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro 145	150	155
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg 165	170	175
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala 180	185	190
Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro 195	200	205
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val 210	215	220
Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys 225	230	235
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn 245	250	255
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly 260	265	270
Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu 275	280	285
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro 290	295	300
Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr 305	310	315
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala 325	330	

(C) INFORMATION FOR SEQ ID NO:64:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Xaa Asn Tyr Gly Gln Val

1	5	10	15
Val Ala Ala Leu			
	20		

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1					5				10					15

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala	Ala	Lys
1				5				10							15
Glu Gly Arg															

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	Phe	Asp	Pro	Ala	Trp	Gly	Pro
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO:61:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp	Pro	Ala	Ser	Ala	Pro	Asp	Val	Pro	Thr	Ala	Ala	Gln	Gln	Thr	Ser
1				5					10						15
Leu	Leu	Asn	Asn	Leu	Ala	Asp	Pro	Asp	Val	Ser	Phe	Ala	Asp		
		20					25						30		

(12) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Gly	Cys	Gly	Asp	Arg	Ser	Gly	Gly	Asn	Leu	Asp	Gln	Ile	Arg	Leu	Arg
1				5				10							15
Arg	Asp	Arg	Ser	Gly	Gly	Asn	Leu								
			20												

(12) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Thr	Gly	Ser	Leu	Asn	Gln	Thr	His	Asn	Arg	Arg	Ala	Asn	Glu	Arg	Lys
1				5					10						15
Asn	Thr	Thr	Met	Lys	Met	Val	Lys	Ser	Ile	Ala	Ala	Gly	Leu	Thr	Ala
			20					25							30
Ala	Ala	Ala	Ile	Gly	Ala	Ala	Ala	Ala	Gly	Val	Thr	Ser	Ile	Met	Ala
			35					40							45
Gly	Gly	Pro	Val	Val	Tyr	Gln	Met	Gln	Pro	Val	Val	Phe	Gly	Ala	Pro
		50					55						60		
Leu	Pro	Leu	Asp	Pro	Ala	Ser	Ala	Pro	Asp	Val	Pro	Thr	Ala	Ala	Gln
			65				70					75			80
Leu	Thr	Ser	Leu	Leu	Asn	Ser	Leu	Ala	Asp	Pro	Asn	Val	Ser	Phe	Ala
					85				90						95
Asn	Lys	Gly	Ser	Leu	Val	Glu	Gly	Gly	Ile	Gly	Gly	Thr	Glu	Ala	Arg
					100				105						110

```

Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro
115                      120                      125

Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala
130                      135                      140

Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr
145                      150                      155                      160

Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala
165                      170                      175

Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Xaa
180                      185

```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
1           5           10           15

Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser
20          25          30

Gly Val Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg
35          40          45

Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser
50          55          60

Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val
65          70          75          80

Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val
85          90          95

Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val
100         105         110

Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu
115         120         125

Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser
130         135         140

Thr Gly Gly Pro
145

```

(2) INFORMATION FOR SEQ ID NO:66:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr
 1           5           10           15

Gly Pro Asp Arg Ser Ala Ser Leu Ser Leu Val Arg His Arg Arg Gln
20           25           30

Gln Arg Asp Ala Leu Cys Leu Ser Ser Thr Gln Ile Ser Arg Gln Ser
35           40           45

Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn
50           55           60

Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu
65           70           75           80

Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Glu
85           90           95

Glu Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser
100          105          110

Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp
115          120          125

Gln Lys Ser Leu Gln Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu
130          135          140

Ser Ala Ala Thr Ser Ser Thr Pro Arg Gln Ala Pro Tyr Glu Leu Asn
145          150          155          160

Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln
165          170          175

Ala Val Val Leu Xaa Val Tyr His Asn Ala Gly Gly Thr His Pro Thr
180          185          190

Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile
195          200          205

Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val
210          215          220

Phe Pro Ile Val Ala Arg
225          230

```

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1      5      10      15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20     25     30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35     40     45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50     55     60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65     70     75     80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85     90     95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100    105    110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115    120    125
Gly Pro Pro Ala
130

```

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
1      5      10      15
Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Leu Ser Asn Pro Pro
20     25     30
Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
35     40     45

```



```

Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa
 30                      55                      60

Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
 65                      70                      75                      80

Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
 85                      90                      95

Ser Glu Arg Lys
100

```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
 1                      5                      10                      15

Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
20                      25                      30

Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp
35                      40                      45

Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
50                      55                      60

Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu
65                      70                      75                      80

Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Gln Arg
85                      90                      95

Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro
100                      105                      110

Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
115                      120                      125

Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg
130                      135                      140

His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Arg Leu Pro Val Arg
145                      150                      155                      160

Asp Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:70:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly
 1             5             10             15

Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg
 20             25             30

Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr
 35             40             45

Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Gln Val Pro
 50             55             60

Arg Gly Arg Lys Glu Ala Val Ala Ala Val Ala Ser Leu Arg
 65             70             75             80

Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly
 85             90             95

Gln Thr Asp Thr Ala Ala Ala Ile Leu Ala Gly Thr Ala Pro Ala Ala
100             105             110

Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr
115             120             125

Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Glu Tyr
130             135             140

Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val
145             150             155             160

Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu
165             170             175

Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu
180             185             190

His Arg Pro Gly Arg Ser Thr Arg Arg Leu Glu Pro Arg Thr Leu Pro
195             200             205

Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe
210             215             220

Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro
225             230             235             240

```

Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro
 245 250 255

Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro
 260 265 270

Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala
 275 280 285

Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu
 290 295 300

Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr
 305 310 315 320

Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Glu Gly Gln
 325 330 335

Val Ser Arg Gln Asn Pro Thr Gly
 340

(2) INFORMATION FOR SEQ ID NO:71:

(a) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala
 1 5 10 15

Leu Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Gln Asp Cys Val Glu
 20 25 30

Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile
 35 40 45

Ile Tyr Arg Gln Arg Arg Ala Glu Leu Arg Thr Ala Lys Ala Leu Leu
 50 55 60

Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Ala Val Thr Val Leu
 65 70 75 80

Arg Glu Arg Tyr Leu Leu His Asp Glu Gln Gly Arg Pro Ala Glu Ser
 85 90 95

Thr Gly Glu Leu Met Asp Arg Ser Ala Arg Cys Val Ala Ala Ala Glu
 100 105 110

Asp Gln Tyr Glu Pro Gly Ser Ser Arg Arg Trp Ala Glu Arg Phe Ala
 115 120 125

Thr Leu Leu Arg Asn Leu Glu Phe Leu Pro Asn Ser Pro Thr Leu Met
 130 135 140
 Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys Phe Val Leu Pro
 145 150 155 160
 Ile Glu Asp Ser Leu Gln Ser Ile Phe Ala Thr Leu Gly Gln Ala Ala
 165 170 175
 Glu Leu Gln Arg Ala Gly Gly Gly Thr Gly Tyr Ala Phe Ser His Leu
 180 185 190
 Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly Thr Ala Ser Gly
 195 200 205
 Pro Val Ser Phe Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser
 210 215 220
 Met Gly Gly Arg Arg Arg Gly Ala Cys Met Ala Val Leu Asp Val Ser
 225 230 235 240
 His Pro Asp Ile Cys Asp Phe Val Thr Ala Lys Ala Glu Ser Pro Ser
 245 250 255
 Glu Leu Pro His Phe Asn Leu Ser Val Gly Val Thr Asp Ala Phe Leu
 260 265 270
 Arg Ala Val Glu Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr
 275 280 285
 Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile
 290 295 300
 Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp
 305 310 315 320
 Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala
 325 330 335
 Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn
 340 345 350
 Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp
 355 360 365
 Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp
 370 375 380
 Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala
 385 390 395 400
 Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu
 405 410 415

```

Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg
    420                      425                      430

Leu Ala Thr Arg Leu Met Arg Arg Ile Gln Gln Ala Ala His Thr Ala
    435                      440                      445

Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp
    450                      455                      460

Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser
    465                      470                      475                      480

Val Ala Pro Thr Gly
    485

```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu
1           5           10           15

Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val
    20           25           30

Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala
    35           40           45

Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His
    50           55           60

Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu
    65           70           75           80

Gly Asp Ala Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Gln Thr Pro
    85           90           95

Thr Pro Thr Ala Ala Val Gln Pro Pro Pro Val Leu Lys Glu Gly Asp
    100          105          110

Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro
    115          120          125

Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn
    130          135          140

Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala
    145          150          155          160

```

Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp
 165 170 175

Cys Ala Pro Ser Asn Glu Thr Leu Val Lys Thr Phe Ser Pro Gly Glu
 180 185 190

Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg
 195 200 205

Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val
 210 215 220

Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn
 225 230 235 240

Gln Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln
 245 250 255

Ala Pro Pro Pro Glu Ser Pro Ala Gln Gly Gly
 260 265

(2) INFORMATION FOR SEQ ID NO:73:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val
 1 5 10 15

Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Gln Val Val Ala
 20 25 30

Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr
 35 40 45

Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala
 50 55 60

Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp
 65 70 75 80

Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Gln
 85 90 95

Gln

(3) INFORMATION FOR SEQ ID NO:74:

- (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala
 1           5           10           15

Cys Gly Gly Gly Thr Asn Ser Ser Ser Ser Gly Ala Gly Gly Thr Ser
 20           25           30

Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser
 35           40           45

Thr Ala Gln Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg
 50           55           60

Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala
 65           70           75           80

Gly Val Thr Gln Phe Leu Asn Asn Glu Thr Asp Phe Ala Gly Ser Asp
 85           90           95

Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Glu Arg
100           105           110

Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro Ile Ala
115           120           125

Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro
130           135           140

Thr Thr Ala Lys Ile Phe Asn Gly Thr Ile Thr Val Trp Asn Asp Pro
145           150           155           160

Gln Ile Gln Ala Leu Asn Ser Gly Thr Asp Leu Pro Pro Thr Pro Ile
165           170           175

Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln
180           185           190

Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser
195           200           205

Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly
210           215           220

Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Glu
225           230           235           240

Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr
245           250           255

```

Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys
 260 265 270

Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu
 275 280 285

Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile
 290 295 300

Val Leu Ala Thr Tyr Gln Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr
 305 310 315 320

Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly
 325 330 335

Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe
 340 345 350

Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser
 355 360

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Asp
 1 5 10 15

Gln Thr His Gln Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val
 20 25 30

Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro
 35 40 45

Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser
 50 55 60

Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg
 65 70 75 80

Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro
 85 90 95

Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg
 100 105 110

Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp
 115 120 125

Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val
 130 135 140
 Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg
 145 150 155 160
 Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly
 165 170 175
 Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala
 180 185 190
 Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val
 195 200 205
 Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg
 210 215 220
 Ala Gly Pro Gln Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro
 225 230 235 240
 Leu Pro Ala Arg Ala Gly Gln Gln Gln Pro Ser Ser Ala Gly Gly Arg
 245 250 255
 Arg Ala Gly Gly Ala Glu Arg Ala Asp Pro Gly Gln Arg Gly Arg His
 260 265 270
 His Gln Gly Gly His Asp Pro Gly Arg Gln Gly Ala Gln Arg Gly Thr
 275 280 285
 Ala Gly Val Ala His Ala Ala Ala Gly Pro Arg Arg Ala Ala Val Arg
 290 295 300
 Asn Arg Pro Arg Arg
 305

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly
 1 5 10 15
 Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys
 20 25 30
 Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala
 35 40 45

Ser Pro Leu Glu Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys
 50 55 60
 Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr
 65 70 75 80
 Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Gln Trp Asn Leu Ser
 85 90 95
 Pro Arg Ala Gln Pro Ser Cys Ala Val Thr Val Glu Ser His Thr His
 100 105 110
 Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Leu Val Gln
 115 120 125
 Glu Glu Gln Pro Ser Asp Met Thr Asn His Pro Arg Tyr Ser Pro Pro
 130 135 140
 Pro Gln Gln Pro Gly Thr Pro Gly Tyr Ala Gln Gly Gln Gln Gln Thr
 145 150 155 160
 Tyr Ser Gln Gln Phe Asp Trp Arg Tyr Pro Pro Ser Pro Pro Pro Gln
 165 170 175
 Pro Thr Gln Tyr Arg Gln Pro Tyr Glu Ala Leu Gly Gly Thr Arg Pro
 180 185 190
 Gly Leu Ile Pro Gly Val Ile Pro Thr Met Thr Pro Pro Pro Gly Met
 195 200 205
 Val Arg Gln Arg Pro Arg Ala Gly Met Leu Ala Ile Gly Ala Val Thr
 210 215 220
 Ile Ala Val Val Ser Ala Gly Ile Gly Gly Ala Ala Ala Ser Leu Val
 225 230 235 240
 Gly Phe Asn Arg Ala Pro Ala Gly Pro Ser Gly Gly Pro Val Ala Ala
 245 250 255
 Ser Ala Ala Pro Ser Ile Pro Ala Ala Asn Met Pro Pro Gly Ser Val
 260 265 270
 Glu Gln Val Ala Ala Lys Val Val Pro Ser Val Val Met Leu Gln Thr
 275 280 285
 Asp Leu Gly Arg Gln Ser Gln Glu Gly Ser Gly Ile Ile Leu Ser Ala
 290 295 300
 Glu Gly Leu Ile Leu Thr Asn Asn His Val Ile Ala Ala Ala Ala Lys
 305 310 315 320
 Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp
 325 330 335
 Gly Arg Thr Ala Pro Phe Thr Val Val Gly Ala Asp Pro Thr Ser Asp

340	345	350
Ile Ala Val Val Arg Val Gln Gly Val Ser Gly Leu Thr Pro Ile Ser 355	360	365
Leu Gly Ser Ser Ser Asp Leu Arg Val Gly Gln Pro Val Leu Ala Ile 370	375	380
Gly Ser Pro Leu Gly Leu Glu Gly Thr Val Thr Thr Gly Ile Val Ser 385	390	400
Ala Leu Asn Arg Pro Val Ser Thr Thr Gly Glu Ala Gly Asn Gln Asn 405	410	415
Thr Val Leu Asp Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn 420	425	430
Ser Gly Gly Ala Leu Val Asn Met Asn Ala Gln Leu Val Gly Val Asn 435	440	445
Ser Ala Ile Ala Thr Leu Gly Ala Asp Ser Ala Asp Ala Gln Ser Gly 450	455	460
Ser Ile Gly Leu Gly Phe Ala Ile Pro Val Asp Gln Ala Lys Arg Ile 465	470	475
Ala Asp Glu Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly 485	490	495
Val Gln Val Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu 500	505	510
Val Val Ala Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val 515	520	525
Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu 530	535	540
Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr 545	550	555
Phe Gln Asp Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly 565	570	575
Lys Ala Glu Gln 580		

(2) INFORMATION FOR SEQ ID NO:77:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu
 1           5           10           15

Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro
 20           25           30

Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro
 35           40           45

Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu
 50           55           60

Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu
 65           70           75           80

Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala Asn Pro Leu Ala
 85           90           95

Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly Val Pro Phe Arg
100           105           110

Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp Asp Trp Ser Asn
115           120           125

Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val Leu Asp Pro Ala
130           135           140

Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn Leu Gln Ala Gln
145           150           155           160

Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys Ile Thr Gly Thr
165           170           175

Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly Ala Lys Ser Ala
180           185           190

Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser His His Leu Val
195           200           205

Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln Leu Thr Gln Ser
210           215           220

Lys Trp Asn Glu Pro Val Asn Val Asp
225           230

```

(x2) INFORMATION FOR SEQ ID NO:78:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala
 1           5           10           15

Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
 20           25           30

Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
 35           40           45

Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
 50           55           60

Pro Arg
 65

```

(xii) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

Val Pro Pro Ala Pro Pro Leu Pro Pro Leu Pro Pro Ser Pro Ile Ser
 1           5           10           15

Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
 20           25           30

Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro
 35           40           45

Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
 50           55           60

Ser Pro Pro Leu Pro
 65

```

(xii) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
 1           5           10           15

```

Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
 20 28 30
 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35 40 45
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp

305	310	315	320
Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln			
	325	330	335
Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly			
	340	345	350
Pro Pro Ala			
355			

(2) INFORMATION FOR SEQ ID NO:81:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Ser	Pro	Lys	Pro	Asp	Ala	Glu	Glu	Gln	Gly	Val	Pro	Val	Ser	Pro	Thr
1				5					10					15	
Ala	Ser	Asp	Pro	Ala	Leu	Leu	Ala	Glu	Ile	Arg	Gln	Ser	Leu	Asp	Ala
			20					25					30		
Thr	Lys	Gly	Leu	Thr	Ser	Val	His	Val	Ala	Val	Arg	Thr	Thr	Gly	Lys
		35				40						45			
Val	Asp	Ser	Leu	Leu	Gly	Ile	Thr	Ser	Ala	Asp	Val	Asp	Val	Arg	Ala
	50				55					60					
Asn	Pro	Leu	Ala	Ala	Lys	Gly	Val	Cys	Thr	Tyr	Asn	Asp	Glu	Gln	Gly
65					70					75				80	
Val	Pro	Phe	Arg	Val	Gln	Gly	Asp	Asn	Ile	Ser	Val	Lys	Leu	Phe	Asp
			85						90				95		
Asp	Trp	Ser	Asn	Leu	Gly	Ser	Ile	Ser	Glu	Leu	Ser	Thr	Ser	Arg	Val
		100						105					110		
Leu	Asp	Pro	Ala	Ala	Gly	Val	Thr	Gln	Leu	Leu	Ser	Gly	Val	Thr	Asn
	115						120					125			
Leu	Gln	Ala	Gln	Gly	Thr	Glu	Val	Ile	Asp	Gly	Ile	Ser	Thr	Thr	Lys
	130					135					140				
Ile	Thr	Gly	Thr	Ile	Pro	Ala	Ser	Ser	Val	Lys	Met	Leu	Asp	Pro	Gly
145					150					155				160	
Ala	Lys	Ser	Ala	Arg	Pro	Ala	Thr	Val	Trp	Ile	Ala	Gln	Asp	Gly	Ser
			165					170					175		
His	His	Leu	Val	Arg	Ala	Ser	Ile	Asp	Leu	Gly	Ser	Gly	Ser	Ile	Gln

180

185

190

Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp
 195 200 205

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
 1 5 10 15
 Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
 20 25 30
 His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
 35 40 45
 Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
 50 55 60
 Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
 65 70 75 80
 Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
 85 90 95
 Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
 100 105 110
 Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
 115 120 125
 Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
 130 135 140
 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
 145 150 155 160
 Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
 165 170 175
 Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
 180 185 190
 Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
 195 200 205
 Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe

210	215	220
Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp		
225	230	235 240
Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg		
	245	250 255
Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln		
	260	265 270
Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys		
	275	280 285

(2) INFORMATION FOR SEQ ID NO:83:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr		
1	5	10 15
Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp		
	20	25 30
Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg		
	35	40 45
Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg		
	50	55 60
Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro		
	65	70 75 80
Arg Glu Ala Leu Ala Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp		
	85	90 95
Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu		
	100	105 110
Gly Gln Gln Phe Met Gln Trp Phe Leu Gln Glu Gln Ile Glu Glu Val		
	115	120 125
Ala Leu Met Ala Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn		
	130	135 140
Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro		
	145	150 155 160
Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu		

165

170

(2) INFORMATION FOR SEQ ID NO:84:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Arg Ala Asp Glu Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser Ile
1           5           10           15
Ala Ala Gly Leu Thr Ala Ala Ala Ala Ile Gly Ala Ala Ala Gly
20           25           30
Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro
35           40           45
Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa
50           55           60
Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp
65           70           75           80
Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Glu Gly Gly Ile
85           90           95
Gly Gly Xaa Glu Gly Xaa Xaa Arg Arg Xaa Gln
100           105

```

(2) INFORMATION FOR SEQ ID NO:85:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

Val Leu Ser Val Pro Val Gly Asp Gly Thr Trp Xaa Arg Val Val Asn
1           5           10           15
Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr
20           25           30
Arg Arg Ala Leu Glu Leu Gln Ala Pro Ser Val Val Xaa Arg Gln Gly
35           40           45
Val Lys Glu Pro Leu Xaa Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
50           55           60
Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr

```

65		70		75		80
Gly Lys Asn Arg Arg Leu Cys Arg Thr Pro Ser Ser Asn Gln Arg Glu						
	85			90		95
Glu Leu Gly Val Arg Trp Ile Pro Arg Ser Arg Cys Ala Cys Val Tyr						
	100			105		110
Val Gly His Arg Ala Arg Arg Gly Thr Tyr His Arg Arg						
	115			120		125

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Cys Asp Ala Val Met Gly Phe Leu Gly Gly Ala Gly Pro Leu Ala Val						
1		5		10		15
Val Asp Gln Gln Leu Val Thr Arg Val Pro Gln Gly Trp Ser Phe Ala						
	20			25		30
Gln Ala Ala Ala Val Pro Val Val Phe Leu Thr Ala Trp Tyr Gly Leu						
	35			40		45
Ala Asp Leu Ala Glu Ile Lys Ala Gly Glu Ser Val Leu Ile His Ala						
	50			55		60
Gly Thr Gly Gly Val Gly Met Ala Ala Val Gln Leu Ala Arg Gln Trp						
	65			70		75
Gly Val Gln Val Phe Val Thr Ala Ser Arg Gly Lys Trp Asp Thr Leu						
	85			90		95
Arg Ala Xaa Xaa Phe Asp Asp Xaa Pro Tyr Arg Xaa Phe Pro His Xaa						
	100			105		110
Arg Ser Ser Xaa Gly						
	115					

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu
 1           5           10           15

Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln
          20           25           30

Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp
      35           40           45

Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe
      50           55           60

His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
      65           70           75           80

Ile Leu Glu Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro
          85           90           95

Pro Ala Ala Gly Gly Gly Ala
          100

```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

Val Gln Cys Arg Val Trp Leu Glu Ile Gln Trp Arg Gly Met Leu Gly
 1           5           10           15

Ala Asp Gln Ala Arg Ala Gly Gly Pro Ala Arg Ile Trp Arg Glu His
      20           25           30

Ser Met Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala
      35           40           45

Thr Lys Glu Gly Arg Gly Ile Val Met Arg Val Pro Leu Glu Gly Gly
      50           55           60

Gly Arg Leu Val Val Glu Leu Thr Pro Asp Glu Ala Ala Ala Leu Gly
      65           70           75           80

Asp Glu Leu Lys Gly Val Thr Ser
          85

```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89.

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
1 5 10 15
Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
20 25 30
Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
35 40 45
Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
50 55 60
Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
65 70 75 80
Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
85 90 95

(2) INFORMATION FOR GEC ID NO: 90:

11) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(3) TYPE: amino acid

(C) STRANDEDNESS: single

(3) TOPOLOGY: linear

(21) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Phe Leu Asn
1 5 10 15

Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
20 25 30

Pro Phe Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln
35 40 45

Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
50 55 60

Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa
65 70 75 80

Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
85 90 95

Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
100 105 110 115

Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
120 125 130

```

```

Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
 130                135                140

Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr
 145                150                155                160

Leu Thr Leu Gln Gly Asp
                165

```

(2) INFORMATION FOR SEQ ID NO:91:

```

(1) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 5 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

Arg Ala Glu Arg Met
 1                5

```

(2) INFORMATION FOR SEQ ID NO:92:

```

(1) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 63 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
 1                5                10                15

Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
 20                25                30

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
 35                40                45

Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
 50                55                60

Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
 65                70                75                80

Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
 85                90                95

Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
100                105                110

Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met

```

115	120	125
Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly		
130	135	140
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro		
145	150	155
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met		
165	170	175
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met		
180	185	190
Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr Ala		
195	200	205
Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly		
210	215	220
Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala		
225	230	235
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Asn Ser Gly		
240	245	250
Arg Arg Asn Gly Gly Pro Ala		
255		

(2) INFORMATION FOR SEQ ID NO:93:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala		
5	10	15
Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly		
20	25	30
Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly		
35	40	45
Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr		
50	55	60
Gln Leu Gly Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro		
65	70	75
Val Gly Val Ala Leu Leu Ala Ala Leu Leu Ala Gly Val Val Leu Val		

85	90	95
Pro Lys Ala Lys Ser His Val Thr Val Val Ala Val Leu Gly Val Leu 100	105	110
Gly Val Phe Leu Met Val Ser Ala Thr Phe Asn Lys Pro Ser Ala Tyr 115	120	125
Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln 130	135	140
Ala Val Ala Ala Val Leu Ala Leu Leu Val Glu Thr Gly Ala Ile Thr 145	150	155
Ala Pro Ala Pro Arg Pro Lys Phe Asp Pro Tyr Gly Gln Tyr Gly Arg 165	170	175
Tyr Gly Gln Tyr Gly Gln Tyr Gly Val Gln Pro Gly Gly Tyr Tyr Gly 180	185	190
Gln Gln Gly Ala Gln Gln Ala Ala Gly Leu Gln Ser Pro Gly Pro Gln 195	200	205
Gln Ser Pro Gln Pro Pro Gly Tyr Gly Ser Gln Tyr Gly Gly Tyr Ser 210	215	220
Ser Ser Pro Ser Gln Ser Gly Ser Gly Tyr Thr Ala Gln Pro Pro Ala 225	230	235
Gln Pro Pro Ala Gln Ser Gly Ser Gln Gln Ser His Gln Gly Pro Ser 245	250	255
Thr Pro Pro Thr Gly Phe Pro Ser Phe Ser Pro Pro Pro Val Ser 260	265	270
Ala Gly Thr Gly Ser Gln Ala Gly Ser Ala Pro Val Asn Tyr Ser Asn 275	280	285
Pro Ser Gly Gly Gln Gln Ser Ser Ser Pro Gly Gly Ala Pro Val 290	295	300

(3) INFORMATION FOR SEQ ID NO:94:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGAAGATGC TGAAATCGAT CGCCGACAGT CTGACCGCCG CGGCTGCMAAT CGGCGCGCGT	60
CGCGCGCGGTG TGACTTCGAT CATGCGTGGC GCGCCCGCTC TATACCGAT GCAGCCGCTC	120


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GTCTTCGGCG CGCCACTGCC GTTGGACCCG GCATCCGCCC CTGACGTCCC GACCGGTCGC 180
CAGTTGACCA GCTGCTCAA CAGCTTCGCC GATCCCAAGC TGTCGTTTGC GAACAAGGCC 240
AGTCTGTGTC AGGGCGGCAT CGGGGGCACC GAGGCGCGCA TCGCGACCA CAAGCTGAAG 300
AAGGCCCCCG AGCAGCGGGA TCTCCGCTG TCGTTACGCG TGACGAACAT CCAGCGCGCG 360
GCGCGCGGTT CGGCGACGCG CGACGTTTCC GTCTCGGGTC CGAGCTCTTC GTCCGCGGTC 420
ACGCGAGAAGC TCACGTTCT GAATCAAGCC GGTGGATGC TGTACGCGCC ATCGCGGATG 480
GAGTTGCTGC AGGCGCGAGG GAACCTGA 507

```

(12) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala
 1             3             10             18
Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro
 20             25             30
Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu
 35             40             45
Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
 50             55             60
Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly
 65             70             75             80
Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg Ile Ala Asp
 85             90             95
His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro Leu Ser Phe
100             105             110
Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp
115             120             125
Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Gln Asn Val
130             135             140
Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met
145             150             155             160

```

Gln Leu Leu Gln Ala Ala Gly Asn
165

(2) INFORMATION FOR SEQ ID NO:96:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

CGTGGCAATG TGGTTGACCG TCGGGGCGCG CGTGGCTCTCG GCAGATCCCG TGGACGGCGT      50
CATTAACACC ACCTGCAATT ACGGGGCGGT AGTAGCTGCG CTCACCGCGA CGGATCCGGG      100
CGCTCCCGCA CAGTTCAACG CTCACCGGT GCGGCACTCG TATTTCGCGA ATTTCCTGCG      150
CGCACCGCGA CTCACGCGCG CTCGCAATGC CGCGCAATTG CAAGCTGTGC CGGGGGCGCG      200
ACAGTACATG GGCCTTGTGC AGTCGGTTCG CGGCTCTGCG AACAACTATT AAGCCCAATC      300
GGGGCCCATC CGCGGACGCG GCATCTCTCG CGGGGCTAGG CCAGATTCCG CGGCTCTCTA      350
ACGGGCCGCA TCGCGCGACC CGGCACGCTC GCGGGGCGTA GCGGAGATTG CCGCGCTCTT      400
CAAGGGGCGG CATCTCTGCG CGAATCTCTG CAGCCCGCGCG GATCCACTAG TTCTAGAGCG      450
CGCGGCAACG CGGTGGAGCT
                                                                                   500

```

(2) INFORMATION FOR SEQ ID NO:97:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```

Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro      1
2           5           10           15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala      20
25           30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser      35
40           45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro      50
55           60
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala      65
70           75           80

```

Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
 85 90 95

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATGACAGAGC ACGAGTGGAA TTCCGGGGGT ATCGAGGCGG CGGCAAGCTC AATCCAGGGA 60
 AATGTCACGT CCATTCATTC CTTCTTTGAC GAGGGGAAGC AGTCCCTGAC CAAGCTCCCA 120
 GCGCCCTGGG CGCGTACCGG TTGGGAAGCC TACC 154

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
 1 5 10 15
 Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
 20 25 30
 Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
 35 40 45
 Glu Ala Tyr
 50

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGTCCGCCA CTTCAGAGTG ACTATGAAGG TCGGCTCCG CTCGAGGAGT TCGTGAACCT 60
 TCGAGGCGCG CGGATACCTG AGGTGCTGCA TTAAGCGACT TTTCAGAAC ATCGTGACGC 120

GCTCGAAGCC CGGCACAGCC GACGGTGGCT CGGCGAGGC GCTGCTCCA AAATCCCTGA	180
GACATTCGNN CGGGGGGGCC TACAAGGAAG TCGGTGCTGA ATTGCGGNG TATCTGGTGG	240
ACCTGTGTGG TCTGAGCCG GACGAAGCG TGTGGACST CG	282

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GATCGTACCC GTGCGAGTGC TCGGCGCCTT TGAGGATGA GTGCACCTGT CTTCTGTGAT	60
GGCATACCCA GAGATGTTGG CGCGGGGGCC TGACACCCCTG CAGAGCATCG GTGCTACCCAC	120
TGTGGCTAGC AATGCCAGTC CGCGGGGGCC GACGACTGGG GTGGTGGCCC CCCTGCCGA	180
TSAGGTGTGG GCGCTGACTG CGCGGCACTT CGCGGCACAT GCGGCGATGT ATCAGTCCCT	240
GAGCGCTGGG GCTGCTGCGA TTCATGACCA GTTCTGTGGC ACCCTTGCCA GCAGGCGGAG	300
CTCTATATGG GCGACTGAAG TCGCCAATGC GCGCGCGGCC AGCTAAGCCA GGAACAGTCG	360
GCACGAGAAA CCACGAGAAA TAGGGACACG TAATGTTGGA TTTCGGGGG TTACCCACCG	420
AGATCAACTC CGGAGGAGTG TACGCGGGCC CGGGTTCGGC CTGGCTGCTG CGCGCGGCTC	480
AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCGGGGC GTGGCGCTTT CAGTCGTTG	540
TCTGGGGTCT GACCGTGGGG TCTGTGATG GTTGTGCGC GGTCTGTGAT GTGGCGGGCG	600
CTTGGCCCTA TGTGGCTGTG ATGAGCGTCA CGCGGGGGCA GCGCGAGCTG ACCCGCGGCC	660
AGGTCCGGGT TCTGTGGCGC GCTTACGAGA CGCGGTATGG GCTGACGCTG CCCCCCGCGG	720
TGATCGCGGA GAACCGTGCT GAACGTATGA TTCTGATAG GACCAACCTC TTGGGGCAAA	780
ACACCGGGCG GATCGCGCTC AACGAGCGCG AATACGGCGA GATGTGGGCT CAGACCGCGG	840
CGCGGATGTT TGGCTACGCT CGCGCGACCG CGACCGGAC GCGGACGTTG CTGCGGTTCT	900
AGGAGGCGCC GGAGATGACC AGCGGGGGTG GGTCTCTCGA GCAGGCGCGC GCGGTGGAGG	960
AGGCTCTCGA CACCGCGCGC GCGAACCACT TGATGAACAA TGTGCCCCAG GCGCTGCAAC	1020
AGCTGGCGCA GCGCACCGAG GGCACCAACG CTTCTTCCAA CTTGGGTGGC CTGTGGAGAA	1080
CGGTCTCGCC GCATCGGTGG CGGATCAGCA ACATGGTGTG GATGCGCAAC AACCAATGT	1140

CGATGACCAA	CTCGGGTGTG	TCGATGACCA	ACACCTTGAG	CTCGATGTTG	AAGGGCTTTG	1200
CTCGGGGGCG	GGCGGGCCAG	GGCTTGCAAA	CCGCGGCGCA	AAACGGGGTC	CGGGCGATGA	1250
GTCTGCTGGG	CAGCTGCTGT	GGTTCTTGGG	GTCTGGGCGG	TGGGTGGCG	GCCAACTTGG	1320
GTGGGGGGCG	CTGGTCTGGT	TCGTTGTGGG	TGCGGCAGGC	CTGGGCGCGG	GCCAACCAAG	1380
CAGTCACCCC	GGGGGGCGGG	GGCTTGCGCG	TGACCAGGCT	GACGAGCGCC	GGGGAAGAG	1440
GGCGGGGCA	GATGCTGGGC	GGGCTGCGGG	TGGGCGAGAT	GGGCGCCAGG	GCCGTGGGTG	1500
GGCTCAGTGG	TGTGCTGGGT	GTTCGGCGCG	GACCTATGT	GATGCCGCAT	TCTCCGGCGG	1560
CGGCTAGGA	GAGGGGGGGG	AGACTGTGCT	TATTTGACCA	GTGATGCGCG	GTCTGGTGT	1620
TTCCGGCGCG	GGCTATGACA	ACAGTCAATG	TGCATGACAA	ATTACAGGTA	TTAGGTCCAG	1680
GTTCAGCAAG	GAGACAGGCA	ACATGGCTTC	ACGTTTTATG	ACGGATCCGC	ACGGGATCGG	1740
GGACATGGCG	GGCGGTTTTG	AGGTGCACGG	CCAGACGGTG	GAGGACGAGG	CTCGCGGAT	1800
GTGGGGCTCC	GGGCAAAACA	TTCCGGTGC	GGGCTGGAGT	GGCATGCGCG	AGGGGAGCTC	1860
GCTAGACACC	ATGGGCGAGA	TGAATCAGGC	GTTCGCAAC	ATCGTGAACA	TGCTGCACGG	1920
GCTGCTGAC	GGGCTGGTTC	GGGACGGCAA	CAACTACGAG	CAGCAAGAGC	AGGCTTCCCA	1980
GGAGATGCTC	AGCAGCTAAC	GTGAGCTGGT	GCAGCACAAT	ACTTTTACAA	GGGAGGAGA	2040
ACAGGTTGGA	TGACCATCAA	CTATCAATTC	GGGGATGTGG	ACGCTCACGG	CGGCATGATC	2100
CGGCTCAGG	CGGGTGGCT	GGAGGGCGAG	CATCAGGCGA	TCATTGGTGA	TGTATTGACC	2160
GGAGTGAAT	TTTGGGGGGG	GGCGGTTCC	GGGGCTGCC	AGGGGTTTAT	TACCGAGTTG	2220
GGCGTAACT	TCCAGGTGAT	GTACGAGCAG	GCCAACGGCC	ACGGGCGAGA	GGTGCAGGCT	2280
GGCGGCAACA	ACATGGGCGA	AACGAGAGCG	GGGCTGGGCT	CCAGCTGGGC	CTGACACCAG	2340
GCCAAGGCGA	GGGAGTGGT	GTACGAGTGA	AGTTGCTGCC	GTGATCTTTC	GGGTGGCAAT	2400
CTAAGTGGTC	AGTCTGGGG	TGTTGGTGGT	TTGCTGGCTG	GGGGTTCCT	CGGTGCTGCT	2460
CAGTCTGCT	GGGCTCGGG	TGAGGACCTC	GAGGCCGAGG	TAGCGCGGTC	CTTGATGCGA	2520
TTCTGTGTGT	TGTTGGGCGA	GGACGGCTCC	GACGAGGCGG	ATGATCGAGG	CGCGGTGGGG	2580
GAAGATGGCC	ACGAGCTCGG	TTGGGGGTCG	TACCTCTCGG	TTGAGGCGTT	CTTGGGGGTT	2640
GTTCGACGAG	ATTGGGCGCC	AGATCTGCTT	GGGGAAGGCG	GTGAACGCCA	GCAGGTGGGT	2700
GGGGCGGGTG	TGAGGTGCT	GGGCGAGCGG	GGGGAGTTTG	TGGGTGAGAG	CTGTGAGTAC	2760
GGGATCATAT	TGGGCAACAA	CTGATTCGGG	GTGGGGCTGG	TCGTAGATGG	AGTGCAGCAG	2820

GGTGCCACG CACGCCAGG AGGCGTTCGG GGTGGCTGCC ATCAGATTGG CTGCGTAGTG	2880
GGTTCTGCAG CGCTGCCAGG CGGTCGCGG CAGGCTGGCG CGGATCGCG CCACUAGGUC	2940
GGCGTGGCGG TCGTGGTGA CCAGCGCGAC CCGGACAGG CCSCGGGCGA CCAGCTGGCG	3000
GAAGAACCCG AGCCAGCGCG CCGGCTCTTC GCGCGAGGTG ACCTGGATGC CCAGGATC	3058

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met	
1 5 10 15	
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp	
20 25 30	
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser	
35 40 45	
Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly	
50 55 60	
Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr	
65 70 75 80	
Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala	
85 90 95	
Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala	
100 105 110	
Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly	
115 120 125	
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met	
130 135 140	
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala	
145 150 155 160	
Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr	
165 170 175	
Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser	
180 185 190	

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 Gln Glu Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240
 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320
 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
 355 360 365
 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
 370 375 380
 Pro His Ser Pro Ala Ala Gly
 385 390

(2) INFORMATION FOR SEQ ID NO:101:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1725 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(3) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GACGTACGCA CCCGCCGTGC AGGGGTGGAG CGTGCTCGGT TTGATCTGCG GGTCAAGGTC	60
ACCTGCTCTG GGGTGTGCGC GGGGTGGATG CAGACTGCTAT CGCGCTCTTT AATGCACTA	120
ATTTCCTTGA AATGCTCTGC AGGTATAGGA CTCACGATT GGTAAATSTA GCGTTCACCC	180

CCTGTTGGGG	TGATTTCGC	CGACCCAGTC	GTACCAACG	CTTGCGTTC	GGCCAGGCG	240
GGCGATCAGA	TGCTTGACT	ACCAATCAAT	CTTGAGCTCC	CGGCGCGATG	CTCGGCTAA	300
ATGAGGAGGA	GCACGGTGT	CTTTCACGCG	GCAACCGAG	ATGTTGGCGG	CGCGCGTGG	360
CGAATTTCCT	TCGCTGGGGG	CAACCTGAA	GGCTAGCAAT	GCCCGCGCAG	CGGTGGCGAC	420
GACTGGGGTG	GTGCCCCGGG	CTGCCGAGGA	GCTGTGCGTG	CTGCTTGGCA	CACAATTCG	480
TACGCATGCG	GGGACGTATC	AGACGGCCAG	CGCCAAGGCC	GGGTGTATCC	ATGAGCACTT	540
TGTGACCAGG	CTGGCCACCA	GCGCTAGTTC	ATATCGCGAC	ACCGAGGCGG	CGAAGCTGT	600
GCTCACCGCG	TAGCTGACCT	GACGCTATTC	GAGCGGAGGG	ATTATCGAAG	TGTTGGATT	660
CGGGGCGTTA	CGACCGGAGA	TCAACTCGCG	GAGGATGTAC	GCGGCGCGGG	GTTCGCGCTC	720
GCTGTGCGCG	CGCGCGAAGA	TGTGGGACAG	GTTGGCGAGT	GACCTGTITT	CGGCGCGCTC	780
GGCGTTTCAG	TGCGTGGTCT	GGGTCTGAC	GTTGGGCTCG	TGGATAGGTT	CGTCGCGCGG	840
TCTGATGGCG	GCGCGCGGCT	CGCGTATGT	GCTGTGATGT	AGGCTCACCG	CGGCGCAGGC	900
CGAGCTGACC	CGCGCCGAGG	TCCGGTTGC	TGCGCGCGGC	TACGAGACAG	CGTATAGGCT	960
GACGCTGCGC	CGCGCGGTGA	TGCGCGAGAA	CGGTACCGAA	GTGATGACGC	TGACGCGAC	1020
CAACCTCTTG	GGGCAAAACA	CGCGCGCGAT	CGAGGCCAAT	CAGGCGCGAT	ACAGCCAGAT	1080
GTGGGCGCAA	GACGCGGAGG	CGATGTATGG	GTACCGCGCG	AGCGCGCGCA	CGGCGACGGA	1140
GGGTTTGGTG	CGCTTGAGGG	ACGCGTCACT	GATCAGCAAC	CGCGCGCGGC	TGCTTGAGCA	1200
GGCGCTCGCG	GTGAGGAGG	CGATCGACAC	CGCGCGCGCG	AACGAGTTGA	TGAACATAT	1260
CGCGCGAGCG	CTGCAAGAGC	TGCGCTAGCG	AGCGCGCGCG	GTGATACCTT	CTTCCAGCT	1320
GGGTGGGCTG	TGAGCGCGGG	TGCGCGCGCA	TCTGTGCGCG	CTCAGCAAGC	TCACTTCAAT	1380
AGCGAACAAC	CACATGTGGA	TGATGCGCAC	GGGTGTGTGG	ATGACCAACA	CGTTCGACTC	1440
GATGTTGAAG	GCTCTAGCTC	CGCGCGCGCG	TCAGGCGCGT	GAAACCGCGG	CGGAAACCGG	1500
GGTCTGGCGG	ATGAGCTGCG	TGCGCAGCGA	GCTGCGTTGG	TGCTTGGGTT	CTTTCGCTCT	1560
GGCGCGTGGG	GTGCGCGCGA	ACTTGGGTCG	GCGCGCGCTG	GTGCTTGGCT	TGTGGGTGCC	1620
GCCAGCATGG	GCGCGCGCGA	ACGAGGCGGT	CACCTCGCGG	GCGCGCGCGC	TGCGCTGAC	1680
CAGCTTGACC	AGCGCGCGCG	AAACCGCGCG	CGGACACATG	CTGGG		1725

(2) INFORMATION FOR SEQ ID NO:104:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1             5             10             15

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
 20             25             30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35             40             45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50             55             60

Leu Met Ala Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65             70             75             80

Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85             90             95

Ala Tyr Gln Thr Ala Tyr Arg Leu Thr Val Pro Pro Pro Val Ile Ala
100             105             110

Glu Asn Arg Thr Gln Leu Met Thr Leu Thr Ala Thr Asn Leu Leu Gly
115             120             125

Gln Asn Thr Pro Ala Ile Glu Ala Asn Gln Ala Ala Tyr Ser Gln Met
130             135             140

Trp Gly Gln Asp Ala Glu Ala Met Tyr Gly Tyr Ala Ala Thr Ala Ala
145             150             155             160

Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr
165             170             175

Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile
180             185             190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
195             200             205

Gln Gln Leu Ala Gln Pro Ala Gln Gly Val Val Pro Ser Ser Lys Leu
210             215             220

Gly Gly Leu Trp Thr Ala Val Ser Pro His Leu Ser Pro Leu Ser Asn
225             230             235             240

Val Ser Ser Ile Ala Asn Asn His Met Ser Met Met Gly Thr Gly Val
245             250             255

```

Ser Met Thr Asn Thr Leu His Ser Met Leu Lys Gly Leu Ala Pro Ala
 260 265 270
 Ala Ala Gln Ala Val Gln Thr Ala Ala Glu Asn Gly Val Trp Ala Met
 275 280 285
 Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu
 290 295 300
 Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser
 305 310 315 320
 Leu Ser Val Pro Pro Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro
 325 330 335
 Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr
 340 345 350
 Ala Pro Gly His Met Leu Gly
 355

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AGTTCAGTGG AGAATGATAC TGACGGGCTG TATCCAGCAT GGCTGAGACA ACCGACCCAC 40
 CTTCGGACCG GGGGACATCG CAGCCGACCG CGATGGCGTT GCGCGCCGAA GCGGAGCCCG 120
 CCGAAGCCGA AGCGCTGGCC GCGCGGCGCC GGGCCCGTGC CGGTCCCGCC CGGTGAAGC 180
 GTGAGGCGCT GCGCATGGCC CGAGCGGAGG ACGAGAAGCT CCGCGAGGAT ATCGACTG 240
 GGAAGACGCC GAGGACTATG ACGACTATGA CCACTATGAG GCGGCAGACC AGGAGGCGCG 300
 ACGGTGGCCA TCGTGGCGAC GCGCGTTGCG GGTCCGGTTA CCAAGACTGT CCAAGATTGC 360
 CATGGCGGCC GCACTGCTCA TCATCTGCGG GTTCACCGGG CTCAGCGGAT ACATTGTGTG 420
 GCAACACCAT GAGGCGACCG AACCGGACGA GCGCGCCCGG GCGTTCCCGG CCGGAGCCAA 480
 GCAAGGTGTC ATCAACATGA CTTCGCTGGA CTTCACCAAG GCCAAAGAAG ACGTCCGCGG 540
 TGTGATCGAC AGCTCCACCG GCGAATTGAG GGATGACTTC CAGCAGCGCG CAGCGCATTT 600
 CACCAAGGTT GTCGAACAGT CCAAGTGGT CACCGAAGGC ACGGTGAAGC CGACAGCGGT 660
 CGATCGATG AACGAGCATT CCGCCGTGGT GCTCGTCGCG GCGACTTCAC GCGTCACCAA 720

TTCCGCTGGG	GGGAAAGAG	AACCACTGC	GTGGCGCTC	AAAGTGACC	TGACCGAAGA	780
GGGGGACAG	TACAGATGT	CGAAGTTGA	GTTCGTACC	TGACCGATGA	CGTACGCGAC	840
GTCAACACCG	AAACCACTGA	CGCCACCGAA	GTGGCTGAGA	TGACTCAGC	CGCAGGCGAA	900
GGCGGTGATT	GGCGACCGA	GGCATTTGAC	ACCGACTCTG	CAACGGATC	TACCGCGCAG	960
AAGGGTCAGC	GGCAGCTGA	CCTGTGCGA	ATGCAGGTTA	CCTTGAACCT	CGTTCCGGTG	1020
ATTCTCATCC	TGCTCATGTT	GATCTCTGGG	GGCGCGACCG	GATGGCTATA	CCTTGAGCAA	1080
TACGACCGGA	TCAGCAGAG	GACTCGCGCG	CGCCCGCTGC	TGCGCTCGCC	CGCGCGCTCTG	1140
ACGGGACCAAT	CGCGCTTTTG	TGTATTGACC	CGACAGCTCG	ACCAAGACTT	CGCTACCGCC	1200
AGGTCCGACC	TGCGCGCGGA	TTTCCTGTCC	TATACGACCA	GTTCACCGAG	CAGATCGTGG	1260
CTCCGCGCGC	CAACAGAGAG	TCACTGAAAG	CGACCGCCAA	GGTGGTCCGC	CGCGCGCTGT	1320
CGGAGCTAGA	TGCGGATTCT	CGCGCTGCTC	TGGTTTTTGT	CGACGAGAGC	ACTACCGAGTA	1380
AGGACAGGCC	CAATCCGTCG	ATGCGCGCCA	GCAGCGTGAT	GGTGACCTTA	CGCAAGGTCTG	1440
ACGGCAATTC	GCTGATCACC	AAGTTCAACC	CGGTTTAGGT	TGCGGTAGGC	GGTGCGCAAG	1500
TGTGACGCGC	GGCGGGGTGG	CTGCTCTGTC	GAGATACCGG	CGTTTCTCGC	GACATCAGCG	1560
GGCGAGCTTC	AAACAGATCT	CGCGCGCTGT	CTAATCGCGC	GGTTATTTTA	AGATTAGTTG	1620
CGACTGTATT	TAGCTGATGT	TGAGATTGTT	CAGCTGGATT	TAGCTTCGCG	CGAGGGCGGC	1680
TGGTGACCTT	TGATCTGGGG	GTGTGACTA	CTTGAGAGAA	TTTGACCTGT	TGCCGACCTT	1740
GTTCGCTGTC	GATGATTGGT	GCTAGTTATG	GGCGAGCGGA	AGGATTTATG	AGTGGTGGGA	1800
CTTCGCGGCG	TTACCAACCG	AGATCAACTC	CGCGAGGATG	TACGCGCGCC	CGGGTTGCGC	1860
CTGCTGTGTC	GGCGCGCGGA	AGATGTGGGA	CAGCGTGGCG	AGTGACCTGT	TTTCGCGCGC	1920
GTGCGCTTT	CAGTGGGTGG	TTTGGGTGCT	GAGGACCGGA	TGCTGGATAG	GTTCGTGCGC	1980
GGGTCTGATG	GTGCGCGCGG	CCTCGCGCTA	TGTGGCGTGG	ATGAGCGTCA	CGCGGGGCGA	2040
GGCGAGCTG	ACCGCGCGCC	AGGTCCGGGT	TGCTCGCGCG	GGCTACGAGA	CGCGGTATGG	2100
GCTGACGCTG	CGCGCGCGCG	TGATCGCGGA	GAACCGTGGT	GACTGATGA	TTCGTGATGC	2160
GACCAACCTC	TTGGGGCGAA	ACACCGCGCG	GATCGCGCTC	AAAGAGGCGC	AATCGGGGGA	2220
GATGTGGGCT	CAAGACCGCG	CGCGGATGTT	TGGCTACCGC	GCCACGCGCG	CGACGGCGAC	2280
GGAGGCTTTC	GTGCGCTTTC	AGGAGCGCGC	ACTGATCAGC	AACCGCGCGC	GGCTCGCTTA	2340
GCAGCGCTTC	CGGCTCGAGG	AGGCGATCGA	CACGCGCGCG	GGGAACCACT	TGATGAACAA	2400

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TGTGCGCGAA GCGCTGCAAC AACTGGCCCA GCCCAGAAA AGCATCTGGC GTTTCGACCA 2460
ACTGAGTGAA CTCTGGAAAG GCACTCTGCC GCACTCTGGC CGGCTCAGCA ACATCTGTTC 2520
GATGCTCAAC AACCACGTGT GATGACCAA GTGGGTGTG TCGATGCCA GCACCTTCCA 2580
CTCAATGTTT AAGCGCTTTC CTCTGGCGGC GCTCAGGCC GTGGAACCG CGGCGCAAAA 2640
CGGGGTCCAG GCGATGAGCT CGCTGGGCGG CAGCTGGGT TCGTGGCTGG GTTCTTGGGG 2700
TGTGGGCGCT GGGGTGGCGG CCAACTTGGG TCGGGCGGCC TCGGTGGTT GTTGTGGGT 2760
GCCGAGGCC TGGGCGCGG CCAACGAGGC GGTACGCGG CGGCGCGGG CGCTCGCGCT 2820
GACGAGCTG ACCGCGCGG CCAAAAGCG CCGCGAGAC ATGCTGGGG GCTACCGCT 2880
GGGCGCACTG ACCAATAGCG GCGCGCGGT CCGCGCGGT AGCAATGCT TCGGATGCC 2940
CGCGCGGGG TACGTAATGC CGGTGTGCT CCGCGCGGG TAAGCGGAT CGGCGCGCA 3000
TGGGCGCGCT GTATGCGGG AGCGATC 3027

```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 2             5             10             15

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Lys Met Trp
20             25             30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
35             40             45

Val Val Trp Gly Leu Thr Thr Gly Ser Trp Ile Gly Ser Ser Ala Gly
50             55             60

Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65             70             75             80

Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
85             90             95

Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
100            105            110

Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly

```

115	120	125
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met		
130	135	140
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Thr Ala Ala		
145	150	155
Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr		
165	170	175
Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile		
180	185	190
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu		
195	200	205
Gln Gln Leu Ala Gln Pro Thr Lys Ser Ile Trp Pro Phe Asp Gln Leu		
210	215	220
Ser Glu Leu Trp Lys Ala Ile Ser Pro His Leu Ser Pro Leu Ser Asn		
225	230	235
Ile Val Ser Met Leu Asn Asn His Val Ser Met Thr Asn Ser Gly Val		
245	250	255
Ser Met Ala Ser Thr Leu His Ser Met Leu Lys Gly Phe Ala Pro Ala		
260	265	270
Ala Ala Gln Ala Val Glu Thr Ala Ala Gln Asn Gly Val Gln Ala Met		
275	280	285
Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu		
290	295	300
Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser		
305	310	315
Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro		
325	330	335
Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr		
340	345	350
Ala Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn		
355	360	365
Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro		
370	375	380
Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly		
385	390	395

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATCGGAGGG AGTGATCACC ATGCTGTGGC ACCCAATGCC ACCGAGTAA ATACCGCACG	60
GCTGATGGCC GGGCGGGGTC CGCTCCCAAT GCTTCGGGTC GCGCGGGGAT GGCAGACCTT	120
TTCCGGGGCT CTGGACCTCT AGCGCGTCGA GTTGACCGGC CGCTGAACT CTCCTGGAGA	180
AGCGTGGACT GAGGTGGCA GGGACAAGGC GCTTCGGGCT GCAACGCGGA TGGTGGTCTG	240
GCTACAAACC GCTCAACAC AGGCCAAGAC CGTTCGGATG CAGCGACGG CCGAAGCGGC	300
GGCATACACC CAGGCGATGC CCAAGAGCGC GTGCGTGGCG GAGATCGGCC CCAACACAT	360
CACCGAGGCC GTCCCTACGG CCAAGCAACT CTTCGGTATC AACAGATCC GATCGCGTT	420
GACCGGATG GATTATTCA TCCCTATGTG GAACCAAGCA GCGCTGGCAA TGGAGTCTA	480
CCAGCGCGAG ACTCGCGTTA ACAGCGTTTT CGAGAAGCTC GAGCGGATGG CTCTGATCTT	540
TGATCCCGGC GCGAGCGAGA GCACGACGAA CCGCATCTTC GGAATCGGCT CCGCTGGCAG	600
CTCAACACCG GTTGGCCAGT TCGCGCGGCG GGTACCCAG ACCCTCGGCC AACTGGGTGA	660
GATGACCGGC CCGATCGAGC AGCTGACCCA CCGCTCGCAG CAGGTGACCT GCTTCTTCAG	720
CGAGTGGGC GCAACCGGCG CGCGCAACCC AGCCGACGAG GAAGCGCGCG AGATCGGCTT	780
GCTGCGCACC AGTCCGCTGT CGAACCATGC GCTGCTGGT GATCAGGCG CCGAGCGCGG	840
TCGCGGCTGT CTGCGCGCGG AGTGCCTACC TGGCGCAGGT GGGTCCTTGA CCGCGACGCC	900
GCTGATGTCT CAGCTGATCG AAAAGCGCGT TGGCGGCTCG GTGATGCGCG CGGCTGCTGC	960
CGGATGTCTG GCGAGCGGTC GCGCGGCTCT GGTGGGTGCG GAGCGGATGC GCGAGGTTGC	1020
GCAATCGGCG GGTCCACCCA GCGCGGCTCT GGTGCGCGCG GCACGCGTCS CCGAGGAGCG	1080
TGAGAGAGAC GACGAGGACG ACTGGGACGA AGAGGACGAC TGGTGAGCTC CCTATATGAC	1140
AACAGACTTC CCGCGCACCG GGGCGGGAAG ACTTGCACAC ATTTTGGCGA GGAAGGTAAA	1200
GAGAGAAACT AGTCCAGCAT GGCAGAGATG AAGACCGATG CGCTACCTT CCGCGAGGAG	1260
GCAGGTAAAT TCGAGCGGAT CTCGCGGAC CTGAAAACCC AGATCGACCA GGTGGAGTGC	1320
ACGCGAGGTT GCTTGCAGGG CCACTGGGCG GCGCGGCGCG GCAAGCGCGC CCGAGCGGCG	1380
GTGGTGGCTT TCGAAGAAAC AGCGAATAAG CAGAAGCAGG AACTCGACCA GATCTCGAGC	1440

AAATATTGCTG AGGCCCGCGT CCAATACTCG AGGCCCGACG AGGAGCAGCA GCAGGCGCTG	1500
TCCTCGCAAA TGGGCTTCTG ACCGGCTAAT ACGAAAGAA ACGGAGCAAA AACATGACAG	1560
AGCAGCAGTG GAATTTCCCG GGTATCGAGG CCGCGGCAAG CGCAATCCAG GGAAAT	1616

(2) INFORMATION FOR SEQ ID NO:108:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTAGTGGATG AGACCATGGC CATTTCCTGC AGTCTCACTG CTTCTGTGTG TGACATTTTG	60
GCAGCGCGGC GGAAACGAGC CACTGGGGTC GAAGAACGGC TGCGCTGCCA TATCGTCGGG	120
AGCTTCATA CTTCTGTGGC GCGGGAAGAG CTTGTGTAG TCGCGGCCA TGACAACCTC	180
TCAGAGTGGC CTCAAACGTA TAAACACGAG AAAGGGCGAG ACCGACGGAA GGTGGAATC	240
GCGGATATCC GTGTTTCGCT ATTCTACCGG AACTCGGCGT TGCGCTATGC GAACATCCCA	300
GTGACCTTTC CTCGCTGGA AGCCATTGGC TGACGGGCTT CGCTGATCGT CCGCGCCAGG	360
TTCTGCAGCG CTTGTGTCAG CTCGGTAGCC GTGGCGTCCC ATTCTTCTG GACACCGCTG	420
TACGCGCTCG AA	432

(2) INFORMATION FOR SEQ ID NO:109:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 168 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met	Leu	Trp	His	Ala	Met	Pro	Pro	Glu	Xaa	Asn	Thr	Ala	Arg	Leu	Met
1				5					10					15	
Ala	Gly	Ala	Gly	Pro	Ala	Pro	Met	Leu	Ala	Ala	Ala	Ala	Gly	Trp	Gln
				20				25					30		
Trp	Leu	Ser	Ala	Ala	Leu	Asp	Ala	Gln	Ala	Val	Glu	Leu	Thr	Ala	Arg
				35			40					45			
Leu	Asn	Ser	Leu	Gly	Glu	Ala	Trp	Thr	Gly	Gly	Gly	Ser	Asp	Lys	Ala
				50			55					60			

Leu Ala Ala Thr Pro Met Val Val Trp Leu Gln Thr Ala Ser Thr
 65 70 75 80
 Gln Ala Lys Thr Arg Ala Met Gln Ala Thr Ala Gln Ala Ala Tyr
 85 90 95
 Thr Gln Ala Met Ala Thr Thr Pro Ser Leu Pro Glu Ile Ala Ala Asn
 100 105 110
 His Ile Thr Gln Ala Val Leu Thr Ala Thr Asn Phe Phe Gly Ile Asn
 115 120 125
 Thr Ile Pro Ile Ala Leu Thr Glu Met Asp Tyr Phe Ile Arg Met Trp
 130 135 140
 Asn Gln Ala Ala Leu Ala Met Glu Val Tyr Gln Ala Glu Thr Ala Val
 145 150 155 160
 Asn Thr Leu Phe Glu Lys Leu Gln Pro Met Ala Ser Ile Leu Asp Pro
 165 170 175
 Gly Ala Ser Gln Ser Thr Thr Asn Pro Ile Phe Gly Met Pro Ser Pro
 180 185 190
 Gly Ser Ser Thr Pro Val Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr
 195 200 205
 Leu Gly Gln Leu Gly Glu Met Ser Gly Pro Met Gln Gln Leu Thr Gln
 210 215 220
 Pro Leu Gln Gln Val Thr Ser Leu Phe Ser Gln Val Gly Gly Thr Gly
 225 230 235 240
 Gly Gly Asn Pro Ala Asp Glu Gln Ala Ala Gln Met Gly Leu Leu Gly
 245 250 255
 Thr Ser Pro Leu Ser Asn His Pro Leu Ala Gly Gly Ser Gly Pro Ser
 260 265 270
 Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly
 275 280 285
 Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val
 290 295 300
 Ala Pro Ser Val Met Pro Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly
 305 310 315 320
 Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser
 325 330 335
 Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln
 340 345 350
 Gln Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp

155

360

365

(2) INFORMATION FOR SEQ ID NO:110:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```

Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
 1             5             10             15

Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
 20             25             30

Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
 35             40             45

Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
 50             55             60

Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly
 65             70             75             80

Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser
 85             90             95

Gln Met Gly Phe
 100

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(2) INFORMATION FOR SEQ ID NO:111:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```

GATGTCGCGG GACCTGAAAA CCCAGATCGA CCAGGTGAG TCGAGCGCAG GTTCGTTGCA      60
GGCCCACTGG CGCGCGCGCG CGGGACGGCC CGCCCGGCC GGGGTGGTCC GCTTCCAAGA      120
AGCAGCCTAAT AAGCGAAGCG AGGAACTCGA CGAGATCTCG ACCAATATTC CTCAGGCGCG      180
CTTCAATATC TCGAGGGCGG ACGAGGAGCA GCAGCAGGCG CTGTCTCTCG AAATGGGCTT      240
CTGACCGCGCT AATACGAAAA GAAACGGAGC AAAACATGTA CAGAGCAGCA GTGGAAATTC      300
GGCGGTATTC AGGCTCGCGC AAGCGCATC CAGGGAAATC TCACGTCCAT TCATTCCTTC      360

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CTTGACGAGG GGAAGCAGTC CCGACCAAG CTCGCA

396

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ile	Ser	Gly	Asp	Leu	Lys	Thr	Gln	Ile	Asp	Gln	Val	Glu	Ser	Thr	Ala
1				5				10					15		
Gly	Ser	Leu	Gln	Gly	Gln	Trp	Arg	Gly	Ala	Ala	Gly	Thr	Ala	Ala	Gln
		20					25					30			
Ala	Ala	Val	Val	Arg	Phe	Gln	Glu	Ala	Ala	Asn	Lys	Gln	Lys	Gln	Glu
		35				40					45				
Leu	Asp	Glu	Ile	Ser	Thr	Asn	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser
	50				55					60					
Arg	Ala	Asp	Glu	Glu	Gln	Gln	Ala	Leu	Ser	Ser	Gln	Met	Gly	Phe	
65				70				75					80		

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GTGGATCCCG ATCCCTGTGT TCGCTATTCT ACCCGAAGTC GCGCTTCCCG TATCGCAACA	80
TCCGAGTGCAC GTTGCCTTCG GTCCGAAGCCA TTCCCTGACC GGTCTGCGTS ATCGTCGCGG	120
CCAGGTTCTG CAGCGCGTTG TTGAGCTCGG TAGCCGTGGC GTCCCATTTT TCGTGGACAC	160
CTTGATACGC CTCGGAACCG CTACCGCCCG AGGCGGCTGC GAGCTTGCTC AGGCACTGCT	240
TCCCTCTCTC AAGGAGGGAA TGAATGGAGC TGACATTTCC CTGGATTGCG CTTCGCCCGG	300
CCTGATACGC CCGGAAATTC CACTGCTGCT CTGTGATGTT TTGCTCGGT TTGTTTTGTT	360
ATTAGCGGGT CAGAACCCCA TTTCGCA	387

(2) INFORMATION FOR SEQ ID NO:114:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CGGCACGAGG ATCTGGTTG GCCCAACGCG GCTGGCGAGG GCTCCGTTCC GGGGCGGAGC	60
TGGCGCGCGG ATGCTTCCTC TGGCCGCGCG CGCGCCCTGA TGATGCGACC AGTTGCTACC	120
TTCCCGACST TTCTTCGCT GTCTGTGCGA TAGCGGTGAC CCGGCGCGCG ACCTGGGGAG	180
TGTTGGGGGG CAGGCGGGGT CGTGTGTTCC GCGGGGAGC CAGACGCTCT GGACGGAAAG	240
GGCGGGGGGT CCGCGATTGG CATCTTTGCC CA	272

(2) INFORMATION FOR SEQ ID NO:115:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Asp	Pro	Val	Asp	Ala	Val	Ile	Asn	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val
1				5					10					15	
Val Ala Ala Leu															
20															

(2) INFORMATION FOR SEQ ID NO:116:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1					5				10				15	

(2) INFORMATION FOR SEQ ID NO:117:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys
1 5 10 15
Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:118:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:119:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:120:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:121:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Asp	Pro	Glu	Pro	Ala	Pro	Pro	Val	Pro	Thr	Thr	Ala	Ala	Ser	Pro	Pro
1				5					10					15	
Ser															

(2) INFORMATION FOR SEQ ID NO:122:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala	Pro	Lys	Thr	Tyr	Xaa	Glu	Glu	Leu	Lys	Gly	Thr	Asp	Thr	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:123:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asp	Pro	Ala	Ser	Ala	Pro	Asp	Val	Pro	Thr	Ala	Ala	Gln	Leu	Thr	Ser
1				5					10					15	
Leu	Leu	Asn	Ser	Leu	Ala	Asp	Pro	Asn	Val	Ser	Phe	Ala	Asn		
		20						25					30		

(2) INFORMATION FOR SEQ ID NO:124:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp	Pro	Pro	Asp	Pro	His	Gln	Xaa	Asp	Met	Thr	Lys	Gly	Tyr	Tyr	Pro
1				5					10					15	
Gly	Gly	Arg	Arg	Xaa	Phe										
		20													

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Asp Pro Gly Tyr Thr Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Xaa Xaa Gly Phe Thr Gly Pro Gln Phe Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Third Residue Can Be Either a Gln or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Xaa Pro Xaa Val Thr Ala Tyr Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Xaa Xaa Xaa Glu Lys Pro Phe Leu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Xaa Asp Ser Glu Lys Ser Ala Thr Ile Lys Val Thr Asp Ala Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Ala Gly Asp Thr Xaa Ile Tyr Ile Val Gly Asn Leu Thr Ala Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Ala Pro Glu Ser Gly Ala Gly Leu Gly Gly Thr Val Gln Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Xaa Tyr Ile Ala Tyr Xaa Thr Thr Ala Gly Ile Val Pro Gly Lys Ile
1 5 10 15

Asn Val His Leu Val
20

(2) INFORMATION FOR SEQ ID NO:133:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: DNA (genomic)

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:133:

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GCACAGCTGT CTTGGCTTTT GCGGTGATCG GTTTCGCTC GCTGGCGGTG GCGGTGGCGG      60
TCACCATCCG ACCGACCGCG GCTTCAAAAC CGGTAGAGGG ACACCAAAAC GCGCAGCCAG      120
GGAAGTTTCAT GCCGTTGTTG CGGACGCAAC AGCAGGCGCC GCTCGCGCGG CTTGCGCGCG      180
ATGATCCGAC CGCTGGATTC CAGGCGCGCA CATTTCGCGC TGTACAGAAC GTGGTTCGCG      240
GGCTGGGTAC CTCACCGCGG GTGGGTGGGA CGCGCGCTTC GCTGCGCGG GAAGCGCGCG      300
CGGTGCGCGG TGTGTGCTT GCCCGGTGTC CAATCGCGGT CCGATCATC ATTGCGCGGT      360
TCCCGGGTGG GCAGCGTGGG ATGCGGACCA TCCCGACCGC ACCCGCGACG ACGCGGGTGA      420
CGACGTCGCG GACGACCGCG CGGACCGCGC CGCGGACCAC GCGCGTGACC ACCCGCGCAA      480
CGACGCGCGC GACGACCGCG GTGACCGCGC CGCGCAAGAC GCGCGCGACG ACCTCGGTGA      540
CGACCGCACG AACGACCGTC GCGCGGAGCA CGGTGCGCGC GACGACGTC GCTCGGACCA      600
CGCTGCGCGC GACGACGTC GTGCGGCA CGCGGACCGC GACGACGTC GCTCGGCAAC      660
CGACGCGACG GCGCGGCA CAACCAACCC AACGATGCGC AACCGGACG CAGACCGTGG      720
CGCGCGACG GGTGGCGCGG GCTCGGACG CGCGGTGCGG TGGCGGCAAC GCGCGGCGCG      780
GGGCGCACTT ATTGCGCGCG TTGTGATCAC GGTGCGCGCT TACTACGCT CGGAGGACAT      840
GGCGGTGAT GCGTGACGCG TGTGCTGCGC CTGTCTCAAC GA      882

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(2) INFORMATION FOR SEQ ID NO:134:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: DNA (genomic)

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CGCTCAACCA ACCGCTGCGC CGCGCCGCGC CGCGGATCC GCGCTGCGCG CCACGCCGCG	60
CGGTGCGCTC GGTGCGCGCG TTGCGCGCTT CGCGCGCGTC GCGCGCGACC GCGTGGGTGC	120
CTAGGCGGCT GTTACGCGCC TGGTTGGCGG GGACCGCGCC GGCACCACTG GTACCGCGCA	180
TGGCGCGGCT GCGCGCGCGC GCACCGTTGC CACCGTTGCC ACCGTTGCCA CGGTTCGCGA	240
CCAGCCACCC GCGCGCACCA CCGCACCGCG CGCGCGCGCC CGCACCGCGC GCGTGGCGCT	300
TGCTGCGCGT ACCGCGCGCA CGCGGTTGC CGCGTCCACC GCCACCGGAA CTACCGCGCG	360
ACGCGCGCGT CGCGCGCGCG CGCGCGCGAC CGCGATTGCC ACCGCGCGCA CGCGCGCGCT	420
GGAGTGGCGC GATTAGCGCA CTGACCGCGC CAACCAAGCG AAGTACTCTC GGTACCGGAG	480
CAGTTCGAGA CGACACGACA GCACGGGGTT GTCGCGCGAC TGGTGAAAT GCGACCGGAT	540
AGCGGCTAGC TGTGGGCTGC GGTCAACCTC GATCATGATC TCGAGGTGAC CGTGACCGCG	600
CGCGCGCGAG GAGGCGCTGA ACTCGCGGTT GAGCGCGATC CGGATCGGTT GCGCGCGTGC	660
CGAGCGCAAT ACCGCGGATC CGCGTGTGCA AGCGCGCGCG AGCGCGCGCT CGGTTCGCGC	720
ACNGTGGTGC GGTGGGCTGC TTACGCGGTT GTCTCGGAAC ACAGGTAGCA GGTCTGCTCC	780
GCGUAGCGCA TCGACCAAGC GTTGGCTCAG CTGCT	815

(2) INFORMATION FOR SEQ ID NO:135:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: DNA (genomic)

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACCAGCGCGC GCGTGAAGTC TCAGATCAGA GAGTCTCGCG ACTCAGCGCG GCGGTTGAGC	60
CTTCTCCGAG AACAACTGCT GAAGATCCTC GCGCGCGAAA CAGCGCTGGA TTGAGCCTC	120
TATGACCGGT TGAACGAGCA GATCATCGCG CAGATTGATA TGGCAGCGCT GCGCTAACAG	180
GTGCGCAAGA TGGTGCAGCT GTATGTCTCG GACTCGGTGT CCGCGATCAG CTTTGGCGAC	240
GGCGCGGTGA TGTGTGAG GAAGGAGCTC GCGGAGAGCC AGTATCGGAT CGAGACGCTG	300
GACGCGATCA CGGTGTTTGG GCGCGCGAGG ATGACAAGCC CTTTCATGCT TGAGATGCTC	360
AAGCGTGAGC GCGCATCCA GCTCTTACCG ACCGACGCGC ACTACCAAGG CGGATCTCA	420

ACACCCGACG TGTATACGC GCGCGCGTC CGTCAGCAAG TTCACCGAC CGACGATCCT	480
GCCTTCTGCC TGTCTTAAAG CAGCGCGATC GTGTGAGGA AGATCTGTAA TCAGCAGGCC	540
TTGATTCCGG CACACACGTC GGGGCAAGAC GTTCTGTAGA GCATCCGCAC GATGAAGCAC	600
TGCTGGGCTT GGTTCGATCG ATCGGCTCTT CTGGCGGAGT TGAACGGGTT CGAGGGAAT	660
GCCGCAAAAG CATACTTCAC CGCGCTGGGG CATCTCTCTT CCGAGGAGTT CGCATTCCAG	720
GGCCGCTGGA CTGGGCGGCC GTTGGACGCG TTCAACTCGA TGCTCAGCCT CGGCTATTGG	780
CTGCTGTACA AGACATCAT AGGGGCGATC GAGCGTCACA GCTTGAACGC GTATATCGGT	840
TTCTTACACC AGGATTCCAG ACGGACGCGA ACCTCTCGTG CCGAATTGGG CAGGAGCTCT	900
GCTGAAACCG CTGGCGGCTT GCTCAGTCCG GTTACGTAAT CGCTCGCGCC CAGGCGCGCC	960
CGCGCGCGCA ATACGACGAG ATCGACACGC GAATTGCGCC CGAGCGGTTT GGAGCGCTGC	1020
ATACCGGCGG CACACTTCAC GGCAGCGAAC AGCGCTGGCA CGTGGCGCGC GCGCGTGTCC	1080
GCGTCTACTT CGACACGCGC CATCACGTAG TCACACGTCG GCGCGACTTC CATTCCTTGC	1140
GTTCGGCAGC AG	1152

(2) INFORMATION FOR SEQ ID NO:136:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: DNA (genomic)

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CTCTGCGGCA TTGGGACAGG TGTACTTGCC GTGTGTGTAN GCCGCATGAG TGCCGACGAC	60
CAGCAATGCG GCAACAGGAC GGATCCCGGT CAACGACGCG ACCCGGTCCA CGTGGCGGAT	120
CGCGTGGAGT CGCGGCTGGG CGGCTCTTTC CTGGGGCAGG GTGATCGGAG GTGTTTCCGC	180
CGTGCTTTGC CGCCATTATG CCGGCGCGCC GCTCGGGCG GCGGTATGG CCGAANTCG	240
ATCGGACAC CCGAGATACG GGTCTGTGCA AGCTTTTGA GCTCGCGCG GGCAGCTTC	300
GGCGGCAATT CTACTAGCGA GAAGTGTGGC CGGATACGGA TGTGACCGAA GTCGCTCGGG	360
TGCAGCCAC GCTCATTGCG GATGCGCGCG ACGATGGCG CTGAGCGAT GTTGTGCGCG	420
TTGCGGACGG CGACGCGGTA GGTGCTCAAG TCGGTCTAC GCTTGGGCTT TTGCGACGG	480

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TCCCGACGCT GGTACGGTT GCGCCCGGAA AGCGCGGGGT CCGGTGCCAT CAGGAATGCC      540
TCACCGCGCG GGCACGAC GCGCAGTGCC GCGCGGATGT CAGCGATCGG GACATCATGC      600
TCGGCTTCAT ACTCTCGAC CAGTCGGCGG AACAGCTCGA TTCGGGACC GCCCA          655

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(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```

Asn Ala Val Val Ala Phe Ala Val Ile Gly Phe Ala Ser Leu Ala Val      1
1          5          10          15
Ala Val Ala Val Thr Ile Arg Pro Thr Ala Ala Ser Lys Pro Val Glu      20
20         25         30
Gly His Gln Asn Ala Gln Pro Gly Lys Phe Met Pro Leu Leu Pro Thr      35
35         40         45
Gln Gln Gln Ala Pro Val Pro Pro Pro Pro Asp Asp Pro Thr Ala      50
50         55         60
Gly Phe Gln Gly Gly Thr Ile Pro Ala Val Gln Asn Val Val Pro Arg      65
65         70         75         80
Pro Gly Thr Ser Pro Gly Val Gly Gly Thr Pro Ala Ser Pro Ala Pro      85
85         90         95
Glu Ala Pro Ala Val Pro Gly Val Val Pro Ala Pro Val Pro Ile Pro      100
100        105        110
Val Pro Ile Ile Ile Pro Pro Phe Pro Gly Trp Gln Pro Gly Met Pro      115
115        120        125
Thr Ile Pro Thr Ala Pro Pro Thr Thr Pro Val Thr Thr Ser Ala Thr      130
130        135        140
Thr Pro Pro Thr Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr      145
145        150        155        160
Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr Thr Pro Pro Thr      165
165        170        175
Thr Pro Val Thr Thr Pro Pro Thr Thr Val Ala Pro Thr Thr Val Ala      180
180        185        190
Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro      195
195        200        205        210

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195	200	205
Ala Thr Ala Thr Pro Thr Thr Val Ala Pro Gln Pro Thr Gln Gln Pro		
210	215	220
Thr Gln Gln Pro Thr Gln Gln Met Pro Thr Gln Gln Gln Thr Val Ala		
225	230	235
Pro Gln Thr Val Ala Pro Ala Pro Gln Pro Pro Ser Gly Gly Arg Asn		
	245	255
Gly Ser Gly Gly Gly Asp Leu Phe Gly Gly Phe		
	260	265

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ile	Asn	Gln	Pro	Leu	Ala	Pro	Pro	Ala	Pro	Pro	Asp	Pro	Pro	Ser	Pro
1				5				10						15	
Pro	Arg	Pro	Pro	Val	Pro	Pro	Val	Pro	Pro	Leu	Pro	Pro	Ser	Pro	Pro
	20							25					30		
Ser	Pro	Pro	Thr	Gly	Trp	Val	Pro	Arg	Ala	Leu	Leu	Pro	Pro	Trp	Leu
	35				40							45			
Ala	Gly	Thr	Pro	Pro	Ala	Pro	Pro	Val	Pro	Pro	Met	Ala	Pro	Leu	Pro
	50				55						60				
Pro	Ala	Ala	Pro	Leu	Pro	Pro	Leu	Pro	Pro	Leu	Pro	Pro	Leu	Pro	Thr
	65			70				75					80		
Ser	His	Pro	Pro	Arg	Pro	Pro	Ala	Pro	Pro	Ala	Pro	Pro	Ala	Pro	Pro
				85				90					95		
Ala	Cys	Pro	Phe	Val	Pro	Val	Pro	Ala	Pro	Pro	Leu	Pro	Pro	Ser	
	100							105					110		
Pro	Pro	Thr	Glu	Leu	Pro	Ala	Asp	Ala	Ala	Cys	Pro	Pro	Ala	Pro	Pro
		115					120				125				
Ala	Pro	Pro	Leu	Ala	Pro	Pro	Ser	Pro	Pro	Ala	Gly	Ser	Ala	Ala	Ile
	130						135				140				
Arg	Ala	Leu	Thr	Gly	Ala	Thr	Ser	Ala	Ser	Thr	Leu	Gly	His	Arg	Ala
	145				150					155				160	

Leu Pro Asp Asp Thr Thr Ala Arg Gly Cys Arg Arg Thr Gly
 165 170

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly
 1 5 10 15
 Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg
 20 25 30
 Asn Arg Arg
 35

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu
 1 5 10 15
 Cys Arg Arg Pro Ala Met Arg Gln Glu His Gly Ser Arg Ser Thr Thr
 20 25 30
 Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu
 35 40 45
 Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala
 50 55 60
 Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp
 65 70 75 80
 Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala
 85 90 95

Gly Gln Leu Arg Arg Gln Phe Tyr
108

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Mycobacterium tuberculosis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR Primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Mycobacterium tuberculosis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CCTGAATTCA GGGCTCGGTT GGGCGGGGCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR Primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Mycobacterium tuberculosis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GGATCTCTGCA GCTCTGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTCTGAATTC AGGCTTGGA ATCTCTGCGA T

31

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAGAGAATTC TCAGAAGGCC ATTGGGAGG ACA

33

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 152..1273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TGTTCTCTCGA CCGCAGGCTG GTGGAGGAAG GGCCACCGA ACAGCTGTTC TCCTGCGGA	60
AGCATCCCGA AACCCCGCGA TACGTGCGG GACTGTCCGG GGAGCTCAAG GACGCCAAGC	120
GGCGAAATTS AAGAGCACAG AAAGGTATGG C GTG AAA ATT CGT TTG CAT ACG	172
Val Lys Ile Arg Leu His Thr	
1 5	
CTG TTG GCC GTG TTG ACC GGT GCG CGS CTG CTG CTA GCA GCG GCG GCG	210
Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Ala Ala Ala Gly	
10 15 20	
TGT GGC TCG AAA CCA CGG AGC GGT TCG CCT GAA ACG GGC GCC GGC GCC	258
Cys Gly Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala	
25 30 35	
GGT ACT GTC GCG ACT ACC GCG GCG TCG TCG CCG GTG ACG TTG GCG SAG	316
Gly Thr Val Ala Thr Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu	
40 45 50 55	
ACC GGT AGC ACG CTG CTC TAC CCG CTG TTC AAC CTG TCG GGT CCG GCC	364
Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala	
60 65 70	
TTT CAC GAG AGG TAT CCG AAC GTC ACG ATC ACC GGT CAG GCG ACC GGT	412
Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Glu Gly Thr Gly	
75 80 85	
TCT GGT GCG GCG ATC GCG CAG GCC GCC GCG GCG ACG GTC AAC ATT GCG	460
Ser Gly Ala Gly Ile Ala Gln Ala Ala Ala Gly Thr Val Asn Ile Gly	
90 95 100	
GCC TCG GAC GCG TAT CTG TCG GAA GGT GAT ATG GCG GCG CAC AAG GCG	508
Ala Ser Asp Ala Tyr Leu Ser Glu Gly Asp Met Ala Ala His Lys Gly	
105 110 115	

CTG ATG AAC ATC GCG CTA GCC ATC TCC GCT CAG CAG GTC AAC TAC AAC Leu Met Asn Ile Ala Leu Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn 120 125 130 135	556
CTG CCC GGA GTG AGC GAG CAC CTC AAG CTG AAC GGA AAA GTC CTG GCG Leu Pro Gly Val Ser Glu His Leu Lys Leu Asn Gly Lys Val Leu Ala 140 145 150	604
GCC ATG TAC CAG GGC ACC ATC AAA ACC TGG GAC GAC GCG CAG ATC GCT Ala Met Tyr Gln Gly Thr Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala 155 160 165	652
GCG CTC AAC CCC GCG GTG AAC CTG CCC GGC ACC GCG GTA GTT CCG CTG Ala Leu Asn Pro Gly Val Asn Leu Pro Gly Thr Ala Val Val Pro Leu 170 175 180	700
CAC GGC TCC GAC GGG TCC GGT GAC ACC TTC TTG TTC ACC CAG TAC CTG His Arg Ser Asp Gly Ser Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu 185 190 195	748
TCC AAG CAA GAT CCC GAG GGC TGG GGC AAG TCG CCC GGC TTC GGC ACC Ser Lys Gln Asp Pro Glu Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr 200 205 210 215	796
ACC GTC GAC TTC CCG GCG GTG CCG GGT GCG CTG GGT GAG AAC GGC AAC Thr Val Asp Phe Pro Ala Val Pro Gly Ala Leu Gly Glu Asn Gly Asn 220 225 230	844
GGC GGC ATG GTG ACC GGT TGC GCC GAG ACA CCG GCG TGC GTG GCG TAT Gly Gly Met Val Thr Gly Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr 235 240 245	892
ATC GGC ATC AGC TTC CTC GAC CAG GCC AGT CAA CCG GGA CTC GGC GAG Ile Gly Ile Ser Phe Leu Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu 250 255 260	940
GCC CAA CTA GGC AAT AGC TCT GGC AAT TTC TTG TTG CCC GAC GCG CAA Ala Gln Leu Gly Asn Ser Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln 265 270 275	988
AGC ATT CAG GCC GCG GCG GCT GGC TTC GCA TCG AAA ACC GCG GCG AAC Ser Ile Gln Ala Ala Ala Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn 280 285 290 295	1036
CAG GCG ATT TCG ATG ATC GAC GGG CCC GCC CCG GAC GCG TAC CCG ATC Gln Ala Ile Ser Met Ile Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile 300 305 310	1084
ATC AAC TAC GAG TAC GCG ATC GTC AAC AAC CCG CAA AAG GAC GCC GCG Ile Asn Tyr Glu Tyr Ala Ile Val Asn Asn Arg Gln Lys Asp Ala Ala 315 320 325	1132
ACC GCG CAG ACC TTG CAG GCA TTT CTG CAC TGG GCG ATC ACC GAC GCG Thr Ala Gln Thr Leu Gln Ala Phe Leu His Trp Ala Ile Thr Asp Gly 330 335 340 345	1180

330	335	340	
AAC AAG GCC TCG TTC CTC GAC CAG GTT CAT TTC CAG CCG CTG CCG CCC			1228
Asp Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro			
345	350	355	
GCG GTG GTG AAG TTG TCT GAC GCG TTG ATC GCG ACG ATT TCC AGC			1273
Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser			
360	365	370	
TAGCCTCGTT GACCAACAGC CGACAGCAAC CTCCCTCGGG CCATCGGGCT GCTTTCGGGA			1333
GCATCTCTGC CCGTCCGGGT GAAGTCGGCC GCGCTGCCCC GGCATCCGG TGGTTGGGTG			1393
GGATAGGTGC GGTGATCCCG CTGCTTGGCC TGGTCTGGGT GCTGGTGGTG CTGGTCATCG			1453
AGGCGATGGG TCGCATCAGG CTCAACGGGT TGCATTTCCT CACCGCCACC GAATGGAATC			1513
CAGGCAACAC CTACGCGGAA ACGTTGTCTA CCGACGCGTC GCCCATCCCG TCGCGCGCTA			1573
CTACGCGCGG TTGCGGTGTA TCGTCGGGAC GCTGGCGACC TCGGCAATCG CCGTGATCAT			1633
CGCGGTCCCG GTCTCTGTAG GAGCGCGCGT GGTGATCTTG GAACGCGTGC CGAAACCGTT			1693
GGCGGAGGCT GTGGGAATAG TCTGGAATT GCTCGCGCGA ATCCCGACGC TGGTCTGGCG			1753
TTTGTGGGGG GCAATGACGT TGGGCGCGTT CATCGCTCAT CACATCGCTC CCGTGATCGC			1813
TCACAACGCT CCGGATGTGC CGGTGCTGAA CTACTTCCGC GCGACCCCGG GCAACGCGGA			1873
GGCATGTG TGTCGCGGTC TGGTGTGGGC GGTGATGGTC GTTCGATTA TCGGCAACAC			1933
CACTCATGAC CTGTTCCGGC AGGTGCGCGT GTTGGCGCGG GACGCGCGGA TCGGGAATTC			1993

(12) INFORMATION FOR SEQ ID NO:148:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(14) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Val	Lys	Ile	Arg	Leu	His	Thr	Leu	Leu	Ala	Val	Leu	Thr	Ala	Ala	Pro
1					5				10					15	
Leu	Leu	Leu	Ala	Ala	Ala	Gly	Cys	Gly	Ser	Lys	Pro	Pro	Ser	Gly	Ser
			20					25					30		
Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	Ala	Ser
			35				40					45			
Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	Pro	Leu

50	55	60
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr		
65	70	75 80
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala		
85	90	95
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly		
100	105	110
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser		
115	120	125
Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys		
130	135	140
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr		
145	150	155 160
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro		
165	170	175
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr		
180	185	190
Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly		
195	200	205
Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly		
210	215	220
Ala Leu Gly Gln Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Gln		
225	230	235 240
Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala		
245	250	255
Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn		
260	265	270
Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe		
275	280	285
Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro		
290	295	300
Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn		
305	310	315 320
Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu		
325	330	335
His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val		
340	345	350

His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
355 360 365

Ile Ala Thr Ile Ser Ser
370

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TGTTCTCTCGA CGCGAGGCTG GTGGAGGAAG GCGCCACCGA ACAGCTGTTG TCGTCGCCGA	60
AGCATCGCGA AACCGGCCGA TACGTCCCGG GACTGTCCGG AGACGTCAAG GACCGCAAGC	120
GCGGAAATTC AAGAGCACAG AAAGGTATGG CGTGAAATTC CGTTTCGATA CGCTGTGTGG	180
CGTGTTGACC GTTGCGCGCG TGCTGCTAGC AGCGGCGCGC TGTGCTCGA AACCAACGAG	240
CGGTGTGCGT GAAACGGGCG CGGGGCGCGG TACTGTGCGG ACTACCGCGG CGTGTGCGCG	300
GGTGACGTTG CGGAGAGCGG GTAGCAGCGT GGTCTACCGG CTGTTCAACG TGTGGGGTCC	360
GGCTTTTCAC GAGAGGTATC CGAAGCTCAC GATCACCGCT CAGGCGACCG GTTCTGTGTC	420
CGGATCGCGG CAGGCGCGCG CGGGGACGGT CAACATTGGG GCTTCGAGCG CCTATCTGTC	480
GGAAAGTGTAT ATGGCGCGCG ACAAGGGGCT GATGAACATC GCGCTAGCGA TCTCGCTTCA	540
GCAGGTCAAC TACAACCTGC CGGAGTGGAG CGAGCACGTC AAGCTGAAGC GAAAGTCTCT	600
GGCGCGCATG TACGAGGGCA CGATCAAAAC GTGGGACGAC CGGAGATCG GTGCGCTCAA	660
CGCGCGCGTG AACCTGCGCG GCACGCGCGT AGTTGCGCTG CGCGGCTCGG ACAGGCTCGG	720
TGACACGCTT TGTTCACCGG AGTACCTGTC CAAGCAAGAT CGGAGCGGCT GGGGCGAGTC	780
GGCGCGCTTC GGCAGCGACG TCGACTTCGG GCGCGTGGCG GTTGCGCTCG GTGAGAACGG	840
CAACGCGCGC ATGGTGACCG GTTGCGCGCA GACACCGCGC TCGGTGCGCT ATATCGGCA	900
CAGCTTCGTC GACGAGGGCA GTCAACGGGG ACTCGCGGAG GCGCAATGAG GCAATAGCTC	960
TGGCAATTC TGTGTGCGCG ACGCGCAAG CATTCAGCGG CGCGCGGCTG GCTTCGCGATC	1020
GAAAGCGCGG GCGAAGCAGG CGATTTCGAT GATCGAGCGG CGCGCGCGCG ACGGCTACCG	1080
GATCATCAAC TACGAGTACG CGATGCTCAA CAACCGCGAA AAGGACGCGG CCACCGCGCA	1140

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GACCTTGCGAG GCATTTCCTGC ACTGGGCGAT CACCGACGGC AACAGGGCTT GGTTCCTCGA 1200
CCAGGTTTAT TTCCAGGCGC TCGCGCCCGC GGTGGTGAAG TTGCTGACG CTTGATGCG 1260
GACGATTTCG AGCTAGCGTC GTTGACGACC ACGCGACAGC AACCTCCGTC GGGCCATGCG 1320
GCTGCTTTTC GGAGCATGCT GCGCCGTCGC GTTGAAGTC GCGCGCTGCG CCGGGCCATC 1380
CGGTGGTTGG GTGGGATAGG TCGGTGATC CCGCTGCTTG CCGTGGTCTT GGTGCTGCTG 1440
GTGCTGGTCA TCGAGGCGAT GGTGGCGATC AGGCTCAACG GGTTCGATTT CTTCACTGGC 1500
ACCGATAGGA ATCAGGCGAA CAGGTAGCGC GAAACCGTTG TCACCGACGC GTCCGCCATC 1560
CGGTGGCGCG CTACTACGGG GCCTTGCCGC TGATCGTCGG GACGCTGGCG ACCTGGCGAA 1620
TCGCCCTGAT CATCGCGGTG CCGGTCTCTG TAGGAGCGCG GCTGGTGATC GTGGAACGGC 1680
TGCCGAACAG GTTGGCGGAG GCTGTGGGAA TACTCTTGGA ATTGCTCGCC GGAATCCCGA 1740
GGGTGGTCTG CGGTTTGTGG GGGGCAATGA CATTGCGGCC GTTCATCGGT CATCATATCG 1800
GTCCGGTGAT GGTGACAAC GCTCCCGATG TCCCGGTGCT GAACACTTGG GCGCGCGACC 1860
CGGCGAACGG GGAGGGCATG TTGGTGTCGG GTCTGTGTTT GCGGGTGATG GTCTTCCCGA 1920
TTATCGCCAC CACCACTCAT GACCTGTTCG GGCAGGTGCC GTGTTGCCC CGGAGGGCGG 1980
CGATCGGGAA TTC

```

(2) INFORMATION FOR SEQ ID NO:150:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids.
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

Met Lys Ile Arg Leu Ala Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1             5             10             15
Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
 20             25             30
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 35             40             45
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 50             55             60
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 65             70             75             80

```

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85 90 95
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Gln Gly
 100 105 110
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 115 120 125
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 130 135 140
 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
 145 150 155 160
 Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 165 170 175
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 195 200 205
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe
 275 280 285
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser

370

(2) INFORMATION FOR SEQ ID NO:151:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(151) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GGTCTTGACC ACCACCTGGG TGTGGAAGTC GGTCCCGGGA TTGAAGTCCA GGTACTGCTG	60
GGTGGGCGCG SCGAACAAT AGCGACAAGC ATCGGAGCAG CCGCGGTAGC GGTGACGGT	120
GTAGCGAAAC GCGAAGCGCG CCGCGTTGGG CACCTTGCTC AGCGCTGATT TGCACACAC	180
CTCTGGGAAG GTGATGCGCT CGAATTGTGG CCGCGGAACG CTCGGGACCA GCGCGATCG	240
CTGCAACCGG GCAGCGCGCG TCGTCAACGG GCATCCCGTT CACCGGACAG GCTTCCCGGG	300
CGCAACGCAT ACCATTATTC GAACAACCGT TCTATACCTT GTCAACGCTG GCGCGTACCG	360
AGCGCGCGAC AGGATGTGAT ATGCGATCTC TCGCCGACAC GACAGGAGCC AGGCGCTTATG	420
ACAGCATTCG GCGTGGAGCC CTACGGGCGG CCGAAGTACC TAGAAATCGC CGGGAAGCGC	480
ATGGCGTATA TCGACGAAGG CAAGGGTGAC GGCATCGTCT TTGAGGACGG CAACCCGACG	540
TGCTCTTACT TGTGGCGCAA CATCATGCGG CACTTGGGAG GGCTGGGCGG GCTGTGTGGT	600
TGCGATCTGA TCGGGATGGG CGCCTCGGAC AAGCTCAGCC CATCGGACCC CGACCGCTAT	660
AGCTATGGCG AGCAACGAGA GTTTTGTCTC GCGCTGTGGG ATCGGCTCGA CCGCGGGCAC	720
CAGCTGTGAC TGTGTCTGCA CGACTGGGGC TCGGGGCTCG GCTTGGACTG GGTCAACGAG	780
CATCGCGACC GAGTGCAGGG GATCGCGCTC ATGGAAGCGA TCGTCACTCC GATGAGCTGG	840
CGCGACTGCG CCGCGGCGGT GCGGGGTGTG TTCCAGGGTT TCGGATCGCC TGAAGGCGAG	900
CGAATGGCGT TCGAGCACAA CATCTTTGTC GAACGGGTGC TCGCCGCGGC GATCGTGGCA	960
CAGCTCAGCG ACGAGGAAAT GAACCACTAT CCGCGGCCAT TCGTGAACGG CCGCGAGGAC	1020
CGTCGCCCCA CGTTGTCTGG GCCACGAAAC GTTCCAATCG ACGGTGAGCC CCGCGAGGTC	1080
GTGCGCTTGG TCAACGAGTA CCGGAGCTGG CTGAGGAAA CCGACATGCC GAAAGTGTTC	1140
ATCAACGCGG AGCGCGCGCG GATCATCACC GCGCGCATCC GTGACTATGT CAGGAGCTGG	1200
CGCAACGAGA CGGAATACAC AGTGCGCGGC GTGCATTTCG TTGAGGAGGA CAGCGATGCG	1260
GTGCTATCGT GGGCGGCGCG TCGGACGCAT CCGCGACCTG GAGCGGCTCT CATTTCACGA	1320

GACCAAGAAT GTGATTTCGG GCGAAGGCGG GCGCCTGCTT GTCAACTCAT AAGACTTCCT	1380
GTTCGGGGCA GAGATTCTCA GGGAAAAGGG GACCAATCGG AGCCGCTTCC TTGCAACGA	1440
GGTCGACAA TATACGTGGC AGGACAAAGG TCTTCTATT TGGCCAGCGA ATTAGTGCT	1500
GCCTTTCTAT GGGTCACATT CGAGGAAGCC GAGCCGATCA GCGGTATCCG ATTGAGACTA	1560
TGGAACGGGT ATCATGAAGG CTTCGATCA TTGGAACAGC GGGGGCTCCT GCGCCCTCGG	1620
ATCATCCGAC AGGGCTGCTC TCACAACGCC CACATGTACT ACGTGTACT AGCGCCGAGC	1680
GCGGATCGGG AGGAGGTGCT GCGCGCTCTG ACGAGCGAAG GTATAGCGCG GGTCTTTTAT	1740
TACGTGCGCG TTCAGGATTC GCGCGCCGCG GGTCTGCT	1777

(2) INFORMATION FOR SEQ ID NO:152:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 124 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAGATTGAAT GGTACGGCTC TCCTTAGCGG CTCGCTCCCG TGAATGCCA TATCACGCAC	60
GGCATGTTTC TGCTGTGCGA CTTTGGCGCC ATGCCCGGAC GTTGTAAAC CCGGGGTTTG	120
ATCAGTAATT CGGGGGAGC GTTGGGGGAA GCGGCGCAGG ATGTGCTGTA CCGCGCGCGC	180
GCGCTGCGCT CAGGCGACCC CTGGATGCTC AGCGCCGGTG CCGGACGTA GCGAGGTTT	240
GCGCGCTGTC GTCCACAGTG GTACTCGGCT CACGACGCGG CGCGGTGCTT GGTGAAGAC	300
CGTGACCGAC GCGCGCGATT CAGA	324

(2) INFORMATION FOR SEQ ID NO:153:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GCGGTACCGC CGCGTTGCGC TGCCACGGGA CCGTACGAC CTGAACCACT TCGCCTCGCG	60
AACGATTGAC GAACCGCTCG TGCGCGGCGT GTGGGTGCTC AAGGTGTGGG GTGATGTGCT	120
CGATGACCGG CGCGCGCAGC GGCCTACG CGTGAAGAC GTCTCGCG CGCGCAGCGA	180

GCACGACTTC CAGCCCGACT CAGTCGGCCT GCTGACCGCT CCTGTCCCTA TGGGTGCTTG	240
GGAAAGCTCCG GTTCGGAGAGC GATTTCGCTT CCTCACTGAC CTCGACGCGC ACGAGCAGCG	300
GTGGGCGCGC TCGAGCGAAC GGCACCGCGG CGAAGTGGAG AACCGCGTGG CGGTGCTCCG	360
GTCTGTATCA ACTTGCAGGC GATCTTGGCG TTCCGCTGGC ACGGTTCCCG CTCGAGCGCG	420
CTGAATCGAC TAGATGAGAG CAGTTGGGCA CGAATCGGCG TGTGTTGCTG AGCAAGACAC	480
GAGTACTGTC ATCACTAATG GATGCACTGG ATGACCGGCC TGATTCAGCA GGACCAATGG	540
AATGCGCGG GGCAAAACGT CTCGGAGATG ATCGGCGTCC CCTCGGAACC CTGCGGTGCT	600
GGCGTCACTC GGACATCGGT CCGGCTCCCG GATCTGTGCT GACGCCAGCG CTGAAGGAGT	660
GGAGCGCGCG GGTGCACGCG CTGCTGGAGC GCGCGCAGAC GGTGCTGCTG CGTAAGGCGG	720
GGATCGCGCA GAAGCGCTTC GAGGTGGCGG CGCACGAGTT GTTGTGCTTC CGGACGCTCG	780
CGCACAGCCA CGCGGAGCGG GTTCGCGCGG AGCACCGCGA CTTGCTGGCG CCGCGCGCGG	840
CGGACAGCAC CGACGAGTGT GTCTACTGCG GCGCGCGAGC GAAAGTTGTT GCGGCACTGC	900
CGGTTAAGCG GCGAGAGGCT CTGGACGCGA TCGAGGATCT GCACATCTGG ACCGCGAGT	960
CGGTGCGCGC CGACCGCGTC GACTTTCGGC CGAAGCAGAA ACTGGCGCTC TTGTTGCTCT	1020
CGGGGATGCC GCTGGCGGAG CCGGTCGCGC TGGCGGCTAG GCGCGAGTAC GCGGTTGCA	1080
CGAGCTGGGT CGAGCTGCGG GTGACGCGCA GCTTGGCGGC GCGGTCGAC GACGAGCGCG	1140
CGCTGCGCGA GGTGCGCGCG CCGGTCGCGG AGGCGCTGGC TTGACTGCGC CGCATCGCTT	1200
CGGTCTGAGC TGTACGCCCA GTCGCGCGTG CGAGTGATCT GCTGTGCTTT CGGTGCTTGC	1260
TGGGTTCAAT TGACGCGCGG GGCACAGCA CGAATGCGCG CGGCATCGTC CCGCGCGCGG	1320
GCGCGCACCG CTACAACC	1338

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CGGCGCGCAC CGGCGGCACC GCGCGTACCG GCGGCAACCG CCGTACCGCC GCTGCTGTGG	60
TGGGCTTCGG CGGAAACGCG GACCGTGGCT TCGCTGCGCG CAAAGCGCGT AACGCGGAA	120
TAGGTGGGCG CGCGGTGACA GCGGCGGTGG CGCGCGACCG GCGCAAGCTG	180

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GCACCGGGCG TCGCGCGCGC GCCCGCAACG AGCGCGGCAG CACCGGCNAAT CCGCGCGTA      240
AGCGCGCGCGA CCGCGCGGATC GCGCGGTGCG CCGCGCGCGG CCGCGCGGCT GCACCGCGCA      300
ACCGCGCGCGA TCGCGCGCAAC C                                                    321

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(2) INFORMATION FOR SEQ ID NO:155:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```

GAAGACTCGG CCGCGCGGTA TCGATCGGCT CCGCGACTAC TTTCGCGGAA CCGCGCGCGC      60
CGCGCGGTGCG GCGTATCATC ACCCGTGGCT ACAGCGCCCA CCGCGCGCGA TCGCTGCTGC      120
CGTTCGCTTC CGAACTCGTC ACTTCGGGCG AAGCGCGAGG GCAAGCGCGA ATCACCAGCG      180
CGGTCCAGCA TTGCGGTGCA AAGATCGTGC TCGAAATCGT GCACGCGCGA CGCTACGCTT      240
ACGACCGACT TCGCGTCAGG CGCTCGCGCA TCAAGCGGCG GATCAGCGCG TTTCGTCGCG      300
GAGCACTATC GCGTCGCGCG GTCGAAGCGA CGATCGCGGA TTTCGCGCGG TCGCGCGAGT      360
TGGCGCGCGA TCGCGGCTAC GACGCGGTGCG AATCATCGG CAGCGAAGCG TATCTGCTCA      420
ATCAGTTGCT GCGCGCGCGC ACCACACAGC GCACGCGACT GTGGCGCGCG ACACCGCGCA      480
ACCGTCGCGG GT                                                    492

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(2) INFORMATION FOR SEQ ID NO:156:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 816 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```

Phe Ala Gln His Leu Val Glu Gly Asp Ala Val Glu Leu Trp Arg Ala
 1             5             10             15

Asn Ala Ala Asp Gln Ala Asp Pro Leu Gln Pro Gly Ser Ala Arg Arg
20             25             30

Gln Arg Ala Ser Arg Ser Pro Arg Arg Leu Ala Gly Pro Asn Ala Tyr
35             40             45

His Tyr Ser Asn Asn Arg Ser Ile Leu Cys Gln Arg Trp Pro Leu Pro

```

50	55	60
Ser Ala Ala Gln Asp Val Ile Cys His Leu Cys Pro His Arg Gln Glu 65 70 75 80		
Pro Gly Leu Met Thr Ala Phe Gly Val Glu Pro Tyr Gly Gln Pro Lys 85 90 95		
Tyr Leu Glu Ile Ala Gly Lys Arg Met Ala Tyr Ile Asp Glu Gly Lys 100 105 110		
Gly Asp Ala Ile Val Phe Gln His Gly Asn Pro Thr Ser Ser Tyr Leu 115 120 125		
Trp Arg Asn Ile Met Pro His Leu Glu Gly Leu Gly Arg Leu Val Ala 130 135 140		
Cys Asp Leu Ile Gly Met Gly Ala Ser Asp Lys Leu Ser Pro Ser Gly 145 150 155 160		
Pro Asp Arg Tyr Ser Tyr Gly Glu Gln Arg Asp Phe Leu Phe Ala Leu 165 170 175		
Trp Asp Ala Leu Asp Leu Gly Asp His Val Val Leu Val Leu His Asp 180 185 190		
Trp Gly Ser Ala Leu Gly Phe Asp Trp Ala Asn Gln His Arg Asp Arg 195 200 205		
Val Gln Gly Ile Ala Phe Met Glu Ala Ile Val Thr Pro Met Thr Trp 210 215 220		
Ala Asp Trp Pro Pro Ala Val Arg Gly Val Phe Gln Gly Phe Arg Ser 225 230 235 240		
Pro Gln Gly Glu Pro Met Ala Leu Glu His Asn Ile Phe Val Glu Arg 245 250 255		
Val Leu Pro Gly Ala Ile Leu Arg Gln Leu Ser Asp Glu Glu Met Asn 260 265 270		
His Tyr Arg Arg Pro Phe Val Asn Gly Gly Glu Asp Arg Arg Pro Thr 275 280 285		
Leu Ser Trp Pro Arg Asn Leu Pro Ile Asp Gly Glu Pro Ala Glu Val 290 295 300		
Val Ala Leu Val Asn Glu Tyr Arg Ser Trp Leu Glu Glu Thr Asp Met 305 310 315 320		
Pro Lys Leu Phe Ile Asn Ala Glu Pro Gly Ala Ile Ile Thr Gly Arg 325 330 335		
Ile Arg Asp Tyr Val Arg Ser Trp Pro Asn Gln Thr Glu Ile Thr Val 340 345 350		

```

Pro Gly Val His Phe Val Gln Glu Asp Ser Asp Gly Val Ser Trp
    355                      360                      365

Ala Gly Ala Arg Gln His Arg Arg Pro Gly Ser Ala Leu Ile Ser Arg
    370                      375                      380

Asp Gln Glu Cys Asp Phe Arg Arg Arg Arg Asp Pro Ala Cys Gln Leu
    385                      390                      395                      400

Ile Arg Leu Pro Ala Pro Gly Arg Asp Ser Gln Gly Lys Gly His Gln
    405                      410                      415

Ser Gln Pro Leu Pro Ser Gln Arg Gly Arg Gln Ile Tyr Val Ala Gly
    420                      425                      430

Gln Arg Ser Ser Tyr Leu Pro Ser Glu Leu Val Ala Ala Phe Leu Trp
    435                      440                      445

Ala Gln Phe Glu Glu Ala Glu Arg Ile Thr Arg Ile Arg Leu Asp Leu
    450                      455                      460

Trp Asn Arg Tyr His Glu Ser Phe Glu Ser Leu Glu Gln Arg Gly Leu
    465                      470                      475                      480

Leu Arg Arg Pro Ile Ile Pro Gln Gly Cys Ser His Asn Ala His Met
    485                      490                      495

Tyr Tyr Val Leu Leu Ala Pro Ser Ala Asp Arg Glu Glu Val Leu Ala
    500                      505                      510

Arg Leu Thr Ser Gln Gly Ile Gly Ala Val Phe His Tyr Val Pro Leu
    515                      520                      525

His Asp Ser Pro Ala Gly Arg Arg
    530                      535

```

(2) INFORMATION FOR SEC ID NO: 157.

(1) SEQUENCE CHARACTERISTICS.

CA) LENGTH: 264 amino acids

(4) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: Linear

(XXI) SEQUENCE DESCRIPTION: SEQ ID NO: 157.

Asn Glu Ser Ala Pro Arg Ser Pro Met Leu Pro Ser Ala Arg Pro Arg
 1 5 10 15
 Tyr Asp Ala Ile Ala Val Leu Leu Asn Glu Met His Ala Gly His Cys
 20 25 30
 Asp Phe Gly Leu Val Gly Pro Ala Pro Asp Ile Val Thr Asp Ala Ala
 35 40 45

Gly Asp Asp Arg Ala Gly Leu Gly Val Asp Glu Gln Phe Arg His Val
 50 55 60
 Gly Phe Leu Glu Pro Ala Pro Val Leu Val Asp Gln Arg Asp Asp Leu
 65 70 75 80
 Gly Gly Leu Thr Val Asp Trp Lys Val Ser Trp Pro Arg Gln Arg Gly
 85 90 95
 Ala Thr Val Leu Ala Ala Val His Glu Trp Pro Pro Ile Val Val His
 100 105 110
 Phe Leu Val Ala Glu Leu Ser Gln Asp Arg Pro Gly Gln His Pro Phe
 115 120 125
 Asp Lys Asp Val Val Leu Gln Arg His Trp Leu Ala Leu Arg Arg Ser
 130 135 140
 Glu Thr Leu Glu His Thr Pro His Gly Arg Arg Pro Val Arg Pro Arg
 145 150 155 160
 His Arg Gly Asp Asp Arg Phe His Glu Arg Asp Pro Leu His Ser Val
 165 170 175
 Ala Met Leu Val Ser Pro Val Glu Ala Glu Arg Arg Ala Pro Val Val
 180 185 190
 Gln His Gln Tyr His Val Val Ala Glu Val Glu Arg Ile Pro Glu Arg
 195 200 205
 Glu Gln Lys Val Ser Leu Leu Ala Thr Ala Ile Ala Val Gly Ser Arg
 210 215 220
 Trp Ala Glu Leu Val Arg Arg Ala His Pro Asp Gln Ile Ala Gly His
 225 230 235 240
 Gln Pro Ala Gln Pro Phe Gln Val Arg His Asp Val Ala Pro Gln Val
 245 250 255
 Arg Arg Arg Gly Val Ala Val Leu Lys Asp Asp Gly Val Thr Leu Ala
 260 265 270
 Phe Val Asp Ile Arg His Ala Leu Pro Gly Asp Phe
 275 280

(1) INFORMATION FOR SEQ ID NO:158:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ATGAACAATGT COTGGGTGGT GGGTCGCAAG GCCTTTGGGC GATTGCGCGG CTACTCCTCC	60
GCATGACAGG CGATGCGCGG TTTTTCGGAT GCGTTGCGCC AAGAGCTGCG GGTATAGCGA	120
ATGCGCTCTT CGGTGATCCA CCGCGCGCTG ACCGAGACAC CGCTGTGGCG CAACGTCGAC	180
CGCGGCGACA TGCGCGCGCG GTTTCGCGAG CTCACGCGCA TTCCCGTTCG CTGGGTGCGG	240
GCAGCGGTGC TTGACGGTGT GCGG	264

(3) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TAGTGGCGGA CGATGACGTC GGGTCGCAAG CCGACGCGTT CAAGCACCAG CGCGACCCAG	60
AAGCCCGTGC GATCCTTACC GCGCAAGCGG TGGGTGACCA CCGCGCGCTC GCGCGCAAGC	120
AGTGTGACCA CAGCAGGTAG CGCGCGCTGT GCTCCATTGC GCGTTGGGAA TTGGCGATAC	180
TGCTGCTCA GTAGCGGGT GCGCGCGTCA TTTATGACT GCGTGGATTG CCGCGACTCG	240
GCGTTGAGAC CGTCAATTGT TAGCAAGCTC TTGAATGCGG TTCTGTGCGG CGCTGACTCG	300
TGGCGCTCAT CATCGCGGAG GTCGGGGAAC GCGAGCAAGT GGAAGTCGAT GCGCGTCGGA	360
ACCGCTGCTG GACCGCGGCG GCGAAGCTTC CCGGACGACC GCAGGTGCGC AAGTTCGCTC	420
ATCCCGACCC GCGCGAGCGT TGCCCGTCTG GCGGAATTGG GCAGGAGGCT GCGGAGCCAC	480
CGCGCATCAC CAAGCAACGC TTCCCGAGTA CCGATGCTCA GTTCCGATC CCGCAGACCA	540
ATCTGCTGCG CGCGCATGCT CAGATCGCGC TGCTGCGTTC ACAAGAACCG CCGCAGATGT	600
GCGAGCGGCT ATCGGAGATT GAACCGCGCA CGCAGTTCTT GATTCGCTGC GCGCTGCTGC	660
ACTATTGCGA GTTTCGCGCG GTCGCGGTAT TCAGCAAGCA TGCGAGTCTC GAAGAACTCG	720
CGCCAGCTAA CCGACGGCGT AGCTCCCGCG GTGACCGCGA CGATCGCGCG GTGATCTTTG	780
CGCGGACGCT CGTACCGCTT GATCCACCGC TTCCGCGTGC CCGCGGGGAG GCGGATCAGG	840
TTATCGACCT CCGCGTATGC CGACGCGCAG CTGGGCGCGT TGCTGAGGCT CAAGAACTTC	900
AGCATCGCGA CCGGACACCA GGTGCGCGAC CTGACCTACG TCGGCGAGCG CGACATCGCG	960
GATACAGCA ACATCGCGCG CTCGAGCGTG TTGCTCAACT ACGACGGTAC GTCCAAACGG	1020

GGCACCACCG	TGGTTTCGCA	CGTACGGACC	GGGTCCGACA	CCATTTTCGT	GGCCCCAGTA	1080
ACCATCGGCG	ACGGCGCGTA	TACCGGGGCC	GGCACAGTGG	TGCGGGAGGA	TGTCCCGCGG	1140
GGGGCGCTGG	CAGTGTGGCG	GGGTCCGCAA	C			1171

(2) INFORMATION FOR SEQ ID NO:160:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 227 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GCAAGGGCGG	CACCGGGCGG	GGCGGCATGA	ACAGGCTCGA	CGCGCTGCTA	GGCGCCCAAG	60
ACGGGGGGCA	AGCGGCGACC	GGCGGCACCG	GGCGCAACCG	CGCGCGCGCG	GGCACCAAGT	120
TCACCGAAGG	CGCGACGCGC	AACGCGCGCA	ACGGCGGTGA	CGCGCGGGTC	GGCGGCAACG	180
GGCGAAGCGG	CGGAACGCGC	GCAGACAACA	GCACCAACCG	CGCGCGCG		227

(2) INFORMATION FOR SEQ ID NO:161:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:161:

CGTGGCCACC	ATGGGCGGGG	AGGGCGGTAG	CGGTGGCGCC	GGCTCTACCC	CAGCGCCCAA	60
GGCGCGCCAC	GGCTTCACTG	CAACGAGCGG	CGGCGACGCG	GGCGACGGCG	GCAACGGCGG	120
CAACTCCCAA	GTGGTCGGCG	GCAACGGCGG	CGACGGCGCG	AATGGCGGCA	ACGGCGGCAG	180
CGCGGGCAGG	GGGGGCAACG	GGGGCGCGCG	CGGCGACGCG	GGCTTTGGTG	GCATGAGTGC	240
CAACGGCACC	ACCGGTGGTG	AAAACGGGCG	AAACGGTAAC	CGGCGCGGCA	ACGGTGGCGC	300
CGGC						304

(2) INFORMATION FOR SEQ ID NO:162:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1439 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GTGGGACGCT GCCGAGGCTG TATAACAAGG ACRACATCGA CCAGCGCCGG CTGCTGTAGC	60
TGATCGACCT ATTTAACAGT GCGCGCTTCA GCGCGCAGGG CGAGCACCGC GCCCGGATC	120
TGATGGGTGA GGTGTACGAA TACTTCTCTG GCAATTTCTG TCGCGCGGAA GCGAAGCGGG	180
GTGGCGAGTT CTTTACCCCG CCCGCGCTTG TCAAGGTGAT CGTGGAGGTC CTGGAGCCGT	240
CGAGTGGGCG GGTGTATGAC CCGTGTCTGG GTTCGGGAGG CATGTTTGTG CAGACCSAGA	300
AGTTTCATCTA CGAACACGAC GCGGATCGGA AGGATGTCTC GATCTATGCG CAGGAAGCCA	360
TTGAGGAGAC CTGGCGGATG CGCAAGATGA ACCTCGCCAT CCACGGCATC GACAACAAGG	420
GGCTCGGCGC CGGATGGAGT GATACCTTGG CCGCGGACCA GCACCCGGAC GTGCAGATGG	480
ACTACGTGAT GCGCAATCGG CGCTTCAACA TCAAGAGCTG GCGCCGCAAC GAGGAAGACC	540
CACGCTGGCG CTTCGTGTGT CCGCGCGGCA ATAAAGGCCAA TACCGCATGG ATTCAACACA	600
TGCTGTACAA CTTGCGCGCG GAGGATCGGG CAGCGCGTGT GATGGCCAAC GGTGTGATGT	660
CGTGGAACTC CAACGGCAAG GCGGATATTC GCGCGCAAAAT CGTGGAGGCG GATTTGTGTT	720
CGTGCATGCT CGCGTTACCT ACCGAGCTGT TCGCGAGCAC CGGATATCCG GTGTGCTGTT	780
GGTTTTTCGC CAATAACAGG GCGCGAGGTA AGCAAGGCTC TATCAACCGG TCGCGGACGG	840
TGCTGTTCAT CGAGCTGCTT GAATGCGCGG ACTTAGTGGG CCGCGCGGAG CGGCGGCTGA	900
CCAACGAGGA GATCTTCCGC ATCGGGGATA CTTTCCACGC GAGCGACGAC ACCGCAACGG	960
CGGCGTCCGG TGGTCCCGCG GGTAAATGGG GCACTGCGCT CAACGCGCGG GCGGCTGCTG	1020
GCGCGGCGCG CGGCAACGCG GGTGTGCGCG GCTGTGCTCT CGGCAACGCT GTGGGCGGCG	1080
ACGCGCGCAA CGGCGCGCAC GCGCGCCACG GCGGCGAGCG CACGACCGGC GCGCGCGCGG	1140
CGAAGGCGCG CAACGCGCAG AGCGGTGCGG CCGGCGCTC AGCGGTGCTC AACCTACCG	1200
CGGCGCACGG CGGCAACGCG GCGAATGCGG GCAACGCGCG CAAGCGCTGC GCGCGCGCGG	1260
GCGCGCACGG CGGTGCGCGG GCGAGCGCGG GCAACGCGCG CCACGCGCGC GGTGCTACCG	1320
GCGCGCGCGG CGGCAAGGCG GCGAAGCGCA CCGCGGTGC CGGCAAGCGC TCGCGGCTCA	1380
TCAACGTCAC GCGCGCGCAC GCGGCGAAGG GCGGCAATGG CGGCAACGCG GCGCAACGCG	1440

(2) INFORMATION FOR SEQ ID NO:163:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single